

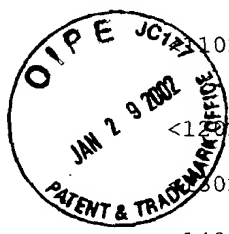
QAG
conclude
NO:70) from the connecting strand 3 from human fibronectin,
PKPSTPPGSS (SEQ ID NO:71) from the upper hinge region of
murine IgG₃, SGGTSGSTSGTGST (SEQ ID NO:72), AGSSTGSSTGPGSTT (SEQ
ID NO:73) or GGSGGAP (SEQ ID NO:74).

QAG
42 (Amended). The construct according to claim 39,
wherein the spacer peptide comprises the amino acid sequence
GTKVHMK (SEQ ID NO:69) from tetranectin, amino acid sequence
PGTSGQQPSVGQQ (SEQ ID NO:70) and GTSGQ (residues 2-6 of SEQ ID
NO:70) from the connecting strand 3 from human fibronectin,
PKPSTPPGSS (SEQ ID NO:71) from the upper hinge region of
murine IgG₃, SGGTSGSTSGTGST (SEQ ID NO:72), AGSSTGSSTGPGSTT
(SEQ ID NO:73) or GGSGGAP (SEQ ID NO:74).

IN THE SEQUENCE LISTING

Please substitute the attached Sequence Listing,
numbered as pages 1-108 for the Sequence Listing previously
submitted.

C1014



SEQUENCE LISTING

<10> GRAVERSEN, Jonas
MOESTRUP, Soren
<110> APOLIPOPROTEINS ANALOGUES
<120> GRAVERSEN1A
<140> US 09/987,107
<141> 2001-11-13
<150> US 60/264,022
<151> 2001-01-26
<150> DK PA2001 00057
<151> 2001-01-15
<150> DK PA2000 01682
<151> 2000-11-10
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Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
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Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp
35 40 45
Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
50 55 60
Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
65 70 75 80
Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
85 90 95
Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
100 105 110

AA11
conf

Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu
115 120 125

Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu
130 135 140

Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg
145 150 155 160

Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala
165 170 175

Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr
180 185 190

His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys
195 200 205

Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser
210 215 220

Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu
225 230 235 240

Asn Thr Gln

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Cys Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala

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Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser	20	25	30
Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu	35	40	45
Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln	50	55	60
Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr	65	70	75
Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala	85	90	95
Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu	100	105	110
Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln	115	120	125
Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro	130	135	140
Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu	145	150	155
Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala	165	170	175
Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu	180	185	190
Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala	195	200	205
Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu	210	215	220
Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys	225	230	235
			240

Leu Asn Thr Gln

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<400> 3

Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
 1 5 10 15

Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
 35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser
 50 55 60

Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu
 65 70 75 80

Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu
 85 90 95

Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr
 100 105 110

Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu
 115 120 125

Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met
 130 135 140

Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp
 145 150 155 160

Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys
 165 170 175

Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu
 180 185 190

His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp
 195 200 205

Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr
 210 215 220

Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys
 225 230 235 240

Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu
 245 250 255

His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu
 260 265 270

Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu
 275 280 285

Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 290 295 300

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 1 5 10 15

Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
 35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Leu Lys Leu Leu Asp Asn
 50 55 60

Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly
 65 70 75 80

Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly
 85 90 95

Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val
 100 105 110

Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu
 115 120 125

Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly
 130 135 140

Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly
 145 150 155 160

Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr
 165 170 175

His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg
 180 185 190

Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His
 195 200 205

Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro
 210 215 220

Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe
 225 230 235 240

Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn
 245 250 255

Thr Gln

<210> 5
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<400> 5

Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala Ile Val Asn
 1 5 10 15

Ala Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
 35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser
 50 55 60

Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu
 65 70 75 80

Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu
 85 90 95

Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr
 100 105 110

Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu
 115 120 125

Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met
 130 135 140

Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp
 145 150 155 160

Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys
 165 170 175

Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu
 180 185 190

His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp
 195 200 205

Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr
 210 215 220

Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys
 225 230 235 240

Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu
 245 250 255

His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu
 260 265 270

Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu
 275 280 285

Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 290 295 300

<210> 6
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<400> 6

Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
 1 5 10 15

Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
 35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Ser Gly His Asp Glu Pro
 50 55 60

Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val
 65 70 75 80

Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly
 85 90 95

Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp
 100 105 110

Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val

115 120 125
 Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg
 130 135 140
 Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro
 145 150 155 160
 Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr
 165 170 175
 Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg
 180 185 190
 Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu
 195 200 205
 Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu
 210 215 220
 Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu
 225 230 235 240
 Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys
 245 250 255
 Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu
 260 265 270
 Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val
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 Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 290 295 300

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 <223> Fibronectin based linker

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<400> 7

Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
 1 5 10 15

Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
 35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Ser Gly Gln Asp Glu Pro
 50 55 60

Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val
 65 70 75 80

Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly
 85 90 95

Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp
 100 105 110

Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val
 115 120 125

Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg
 130 135 140

Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro
 145 150 155 160

Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr
 165 170 175

Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg
 180 185 190

Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu
 195 200 205

Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu
 210 215 220

Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu
 225 230 235 240

Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys
 245 250 255

Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu
 260 265 270

Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val
 275 280 285

Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
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Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala Ile Val Asn
1 5 10 15

Ala Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Ser Gly Gln Asp Glu Pro
50 55 60

Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val
65 70 75 80

Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly
85 90 95

Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp
100 105 110

Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val
115 120 125

Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg
130 135 140

Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro
145 150 155 160

Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr
165 170 175

Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg
180 185 190

Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu
195 200 205

Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu

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210                215                220

Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu
225                230                235                240

Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys
                245                250                255

Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu
                260                265                270

Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val
                275                280                285

Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
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Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
1                5                10                15

Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
                20                25                30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
                35                40                45

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Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Lys Val His Met Lys Asp
 50 55 60

Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val
 65 70 75 80

Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe
 85 90 95

Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn
 100 105 110

Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly
 115 120 125

Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly
 130 135 140

Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val
 145 150 155 160

Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu
 165 170 175

Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly
 180 185 190

Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly
 195 200 205

Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr
 210 215 220

His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg
 225 230 235 240

Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His
 245 250 255

Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro
 260 265 270

Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe
 275 280 285

Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn
 290 295 300

Thr Gln
 305

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Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
 1 5 10 15

Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
 35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Lys Val His Met Lys Asp
 50 55 60

Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val
 65 70 75 80

Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe

85	90	95
Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn 100 105 110		
Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly 115 120 125		
Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly 130 135 140		
Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val 145 150 155 160		
Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu 165 170 175		
Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly 180 185 190		
Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly 195 200 205		
Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr 210 215 220		
His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg 225 230 235 240		
Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His 245 250 255		
Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro 260 265 270		
Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe 275 280 285		
Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn 290 295 300		
Thr Gln 305		

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 <223> Mutagen

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<400> 11

Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala Ile Val Asn
 1 5 10 15

Ala Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
 35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Lys Val His Met Lys Asp
 50 55 60

Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val
 65 70 75 80

Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe
 85 90 95

Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn
 100 105 110

Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly
 115 120 125

Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly
 130 135 140

Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val
 145 150 155 160

Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu
 165 170 175

Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly
 180 185 190

Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly
 195 200 205

Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr
 210 215 220

His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg
 225 230 235 240

Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His
 245 250 255

Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro
 260 265 270

Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe
 275 280 285

Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn
 290 295 300

Thr Gln
 305

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 <213> Homo sapiens

<400> 12

Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
 1 5 10 15

Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
 20 25 30

Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
 35 40 45

Val Cys Leu
 50

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Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
 1 5 10 15

Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
 20 25 30

Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
35 40 45

Ala Leu Gln Thr Val Ser Leu Lys Gly Ser
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Gly Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly Cys
1 5 10 15

Pro Lys Pro Pro Glu Ile Ala His Gly Tyr Val Glu His Ser Val Arg
20 25 30

Tyr Gln Cys Lys Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly Val
35 40 45

Tyr Thr Leu Asn Asn Glu Lys Gln Trp Ile Asn Lys Ala Val Gly Asp
50 55 60

Lys Leu Pro Glu Cys Glu Ala Val Ala Gly Lys Pro Lys Asn Pro Ala
65 70 75 80

Asn Pro Val Gln Arg Ser Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg
85 90 95

Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly
100 105 110

Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu
115 120 125

Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser
 130 135 140

Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn
 145 150 155 160

Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu
 165 170 175

Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys
 180 185 190

Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu
 195 200 205

Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln
 210 215 220

Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala
 225 230 235 240

His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu
 245 250 255

Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly
 260 265 270

Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr
 275 280 285

Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu
 290 295 300

Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu
 305 310 315 320

Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 325

<210> 15

<211> 267

<212> PRT

<213> Homo sapiens

<400> 15

Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
 1 5 10 15

Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp
 20 25 30

Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp
 35 40 45

Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
 50 55 60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
 65 70 75 80

Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
 85 90 95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
 100 105 110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
 115 120 125

Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
 130 135 140

Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu
 145 150 155 160

Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala
 165 170 175

Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
 180 185 190

Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
 195 200 205

Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu
 210 215 220

Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
 225 230 235 240

Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
 245 250 255

Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 260 265

<210> 16
 <211> 267
 <212> PRT
 <213> *Macaca fascicularis*

<400> 16

Met Lys Ala Thr Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
 1 5 10 15

Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Thr Pro Trp
 20 25 30

Asp Arg Val Lys Asp Leu Val Thr Val Tyr Val Glu Ala Leu Lys Asp
 35 40 45

Ser Gly Lys Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
 50 55 60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
 65 70 75 80

Val Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
 85 90 95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
 100 105 110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
 115 120 125

Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
 130 135 140

Pro Leu Arg Ala Glu Leu His Glu Gly Thr Arg Gln Lys Leu His Glu
 145 150 155 160

Leu His Glu Lys Leu Ser Pro Leu Gly Glu Glu Val Arg Asp Arg Ala
165 170 175

Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
180 185 190

Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
195 200 205

Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Ser Glu His Leu
210 215 220

Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
225 230 235 240

Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
245 250 255

Leu Glu Glu Tyr Thr Lys Lys Leu Ser Thr Gln
260 265

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<210> 17
<211> 265
<212> PRT
<213> Bos Taurus
```

<400> 17

Met Lys Ala Val Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
1 5 10 15

Gln Ala Arg His Phe Trp Gln Gln Asp Asp Pro Gln Ser Ser Trp Asp
20 25 30

Arg Val Lys Asp Phe Ala Thr Val Tyr Val Glu Ala Ile Lys Asp Ser
35 40 45

Gly Arg Asp Tyr Val Ala Gln Phe Glu Ala Ser Ala Leu Gly Lys Gln
50 55 60

Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Thr Leu Ala Ser Thr Leu
65 70 75 80

Ser Lys Val Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp
85 90 95

Asn Leu Glu Lys Glu Thr Ala Ser Leu Arg Gln Glu Met His Lys Asp
 100 105 110

Leu Glu Glu Val Lys Gln Lys Val Gln Pro Tyr Leu Asp Glu Phe Gln
 115 120 125

Lys Lys Trp His Glu Glu Val Glu Ile Tyr Arg Gln Lys Val Ala Pro
 130 135 140

Leu Gly Glu Glu Phe Arg Glu Gly Ala Arg Gln Lys Val Gln Glu Leu
 145 150 155 160

Gln Asp Lys Leu Ser Pro Leu Ala Gln Glu Leu Arg Asp Arg Ala Arg
 165 170 175

Ala His Val Glu Thr Leu Arg Gln Gln Leu Ala Pro Tyr Ser Asp Asp
 180 185 190

Leu Arg Gln Arg Leu Thr Ala Arg Leu Glu Ala Leu Lys Glu Gly Gly
 195 200 205

Gly Ser Leu Ala Glu Tyr His Ala Lys Ala Ser Glu Gln Leu Lys Ala
 210 215 220

Leu Gly Glu Lys Ala Lys Pro Val Leu Glu Asp Leu Arg Gln Gly Leu
 225 230 235 240

Leu Pro Val Leu Glu Ser Leu Lys Val Ser Ile Leu Ala Ala Ile Asp
 245 250 255

Glu Ala Ser Lys Lys Leu Asn Ala Gln
 260 265

<210> 18
 <211> 265
 <212> PRT
 <213> Sus scrofa

<400> 18

Met Lys Ala Val Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
 1 5 10 15

Gln Ala Arg His Phe Trp Gln Gln Asp Asp Pro Gln Ser Pro Trp Asp

20	25	30
Arg Val Lys Asp Phe Ala Thr Val Tyr Val Asp Ala Ile Lys Asp Ser		
35	40	45
Gly Arg Asp Tyr Val Ala Gln Phe Glu Ala Ser Ala Leu Gly Lys His		
50	55	60
Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Leu Gly Ser Thr Phe		
65	70	75
80		
Thr Lys Val Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp		
85	90	95
Asn Leu Glu Lys Glu Thr Glu Ala Leu Arg Gln Glu Met Ser Lys Asp		
100	105	110
Leu Glu Glu Val Lys Lys Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln		
115	120	125
Asn Lys Trp Gln Glu Glu Met Glu Thr Tyr Arg Gln Lys Met Ala Pro		
130	135	140
Leu Gly Ala Glu Phe Arg Glu Gly Ala Arg Gln Lys Val Gln Glu Leu		
145	150	155
160		
Gln Glu Lys Leu Ser Pro Leu Ala Glu Glu Leu Arg Asp Arg Leu Arg		
165	170	175
Ala His Val Glu Ala Leu Arg Gln His Val Ala Pro Tyr Ser Asp Asp		
180	185	190
Leu Arg Gln Arg Met Ala Ala Arg Phe Glu Ala Leu Lys Glu Gly Gly		
195	200	205
Gly Ser Leu Ala Glu Tyr Gln Ala Lys Ala Gln Glu Gln Leu Lys Ala		
210	215	220
Leu Gly Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu		
225	230	235
240		
Leu Pro Val Leu Glu Asn Leu Lys Val Ser Ile Leu Ala Ala Ile Asp		
245	250	255

Glu Ala Ser Lys Lys Leu Asn Ala Gln
 260 265

<210> 19
 <211> 266
 <212> PRT
 <213> Canis familiaris

<400> 19

Met Lys Ala Ala Leu Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
 1 5 10 15

Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Gln Ser Pro Trp Asp
 20 25 30

Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Ala Val Lys Asp Ser
 35 40 45

Gly Arg Asp Tyr Val Ala Gln Phe Glu Ala Ser Ala Leu Gly Lys Gln
 50 55 60

Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Leu Ser Ser Thr Val
 65 70 75 80

Thr Lys Leu Arg Glu Gln Ile Gly Pro Val Thr Gln Glu Phe Trp Asp
 85 90 95

Asn Leu Glu Lys Glu Thr Glu Val Leu Arg Gln Glu Met Ser Lys Asp
 100 105 110

Leu Glu Glu Val Lys Gln Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln
 115 120 125

Lys Lys Trp Gln Glu Glu Val Glu Leu Tyr Arg Gln Lys Val Ala Pro
 130 135 140

Leu Gly Ser Glu Leu Arg Glu Gly Ala Arg Gln Lys Leu Gln Glu Leu
 145 150 155 160

Gln Glu Lys Leu Ser Pro Leu Ala Glu Glu Leu Arg Asp Arg Ala Arg
 165 170 175

Thr His Val Asp Ala Leu Arg Ala Gln Leu Ala Pro Tyr Ser Asp Asp
 180 185 190

Leu Arg Glu Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Gly Gly
 195 200 205

Gly Ala Ser Leu Ala Glu Tyr His Ala Arg Ala Ser Glu Gln Leu Ser
 210 215 220

Ala Leu Gly Glu Lys Ala Arg Pro Ala Leu Glu Asp Leu Arg Gln Gly
 225 230 235 240

Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Leu Leu Ala Ala Ile
 245 250 255

Asp Glu Ala Thr Lys Lys Leu Asn Ala Gln
 260 265

<210> 20

<211> 266

<212> PRT

<213> Oryctolagus cuniculus

<400> 20

Met Lys Ala Val Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
 1 5 10 15

Gln Ala Arg His Phe Trp Gln Arg Asp Glu Pro Arg Ser Ser Trp Asp
 20 25 30

Lys Ile Lys Asp Phe Ala Thr Val Tyr Val Asp Thr Val Lys Asp Ser
 35 40 45

Gly Arg Glu Tyr Val Ala Gln Phe Glu Ala Ser Ala Phe Gly Lys Gln
 50 55 60

Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Leu Ser Ser Thr Val
 65 70 75 80

Ser Lys Leu Gln Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp
 85 90 95

Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Glu Glu Met Asn Lys Asp
 100 105 110

Leu Gln Glu Val Arg Gln Lys Val Gln Pro Tyr Leu Asp Glu Phe Gln

115 120 125
 Lys Lys Trp Gln Glu Glu Val Glu Arg Tyr Arg Gln Lys Val Glu Pro
 130 135 140
 Leu Gly Ala Glu Leu Arg Glu Ser Ala Arg Gln Lys Leu Thr Glu Leu
 145 150 155 160
 Gln Glu Lys Leu Ser Pro Leu Ala Glu Glu Leu Arg Asp Ser Ala Arg
 165 170 175
 Thr His Val Asp Thr Leu Arg Thr Lys Leu Ala Pro Tyr Ser Asn Glu
 180 185 190
 Leu Gln Gln Arg Leu Ala Ala Arg Leu Glu Ser Ile Lys Glu Gly Gly
 195 200 205
 Gly Ala Ser Leu Ala Glu Tyr Gln Ala Lys Ala Arg Glu His Leu Ser
 210 215 220
 Val Leu Ser Glu Lys Ala Arg Pro Ala Leu Glu Asp Leu Arg Gln Gly
 225 230 235 240
 Leu Leu Pro Val Leu Glu Ser Phe Lys Ala Ser Val Gln Asn Val Leu
 245 250 255
 Asp Glu Ala Thr Lys Lys Leu Asn Thr Gln
 260 265

 <210> 21
 <211> 265
 <212> PRT
 <213> Tupaia glis belangeri

 <400> 21

 Met Lys Ala Val Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
 1 5 10 15

 Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Gln Ser Ser Trp Asp
 20 25 30

 Arg Val Arg Asp Leu Ala Asn Val Tyr Val Asp Ala Val Lys Glu Ser
 35 40 45

Gly Arg Glu Tyr Val Ser Gln Leu Glu Ala Ser Ala Leu Gly Lys Gln
 50 55 60

Leu Asn Leu Lys Leu Val Asp Asn Trp Asp Thr Leu Gly Ser Thr Phe
 65 70 75 80

Gln Lys Val His Glu His Leu Gly Pro Val Ala Gln Glu Phe Trp Glu
 85 90 95

Lys Leu Glu Lys Glu Thr Glu Glu Leu Arg Arg Glu Ile Asn Lys Asp
 100 105 110

Leu Glu Asp Val Arg Gln Lys Thr Gln Pro Phe Leu Asp Glu Ile Gln
 115 120 125

Lys Lys Trp Gln Glu Asp Leu Glu Arg Tyr Arg Gln Lys Val Glu Pro
 130 135 140

Leu Ser Ala Gln Leu Arg Glu Gly Ala Arg Gln Lys Leu Met Glu Leu
 145 150 155 160

Gln Glu Gln Val Thr Pro Leu Gly Glu Asp Leu Arg Asp Ser Val Arg
 165 170 175

Ala Tyr Ala Asp Thr Leu Arg Thr Gln Leu Ala Pro Tyr Ser Glu Gln
 180 185 190

Met Arg Lys Thr Leu Gly Ala Arg Leu Glu Ala Ile Lys Glu Gly Gly
 195 200 205

Ser Ala Ser Leu Ala Glu Tyr His Ala Lys Ala Ser Glu Gln Leu Ser
 210 215 220

Ala Leu Gly Glu Lys Ala Lys Pro Val Leu Glu Asp Ile His Gln Gly
 225 230 235 240

Leu Met Pro Met Trp Glu Ser Phe Lys Thr Gly Val Leu Asn Val Ile
 245 250 255

Asp Glu Ala Ala Lys Lys Leu Thr Ala
 260 265

<210> 22
 <211> 264

<212> PRT

<213> Mus musculus

<400> 22

Met Lys Ala Val Val Leu Ala Val Ala Leu Val Phe Leu Thr Gly Ser
 1 5 10 15

Gln Ala Trp His Val Trp Gln Gln Asp Glu Pro Gln Ser Gln Trp Asp
 20 25 30

Lys Val Lys Asp Phe Ala Asn Val Tyr Val Asp Ala Val Lys Asp Ser
 35 40 45

Gly Arg Asp Tyr Val Ser Gln Phe Glu Ser Ser Ser Leu Gly Gln Gln
 50 55 60

Leu Asn Leu Asn Leu Leu Glu Asn Trp Asp Thr Leu Gly Ser Thr Val
 65 70 75 80

Ser Gln Leu Gln Glu Arg Leu Gly Pro Leu Thr Arg Asp Phe Trp Asp
 85 90 95

Asn Leu Glu Lys Glu Thr Asp Trp Val Arg Gln Glu Met Asn Lys Asp
 100 105 110

Leu Glu Glu Val Lys Gln Lys Val Gln Pro Tyr Leu Asp Glu Phe Gln
 115 120 125

Lys Lys Trp Lys Glu Asp Val Glu Leu Tyr Arg Gln Lys Val Ala Pro
 130 135 140

Leu Gly Ala Glu Leu Gln Glu Ser Ala Arg Gln Lys Leu Gln Glu Leu
 145 150 155 160

Gln Gly Arg Leu Ser Pro Val Ala Glu Glu Phe Arg Asp Arg Met Arg
 165 170 175

Thr His Val Asp Ser Leu Arg Thr Gln Leu Ala Pro His Ser Glu Gln
 180 185 190

Met Arg Glu Ser Leu Ala Gln Arg Leu Ala Glu Leu Lys Ser Asn Pro
 195 200 205

Thr Leu Asn Glu Tyr His Thr Arg Ala Lys Thr His Leu Lys Thr Leu

210 215 220
 Gly Glu Lys Ala Arg Pro Ala Leu Glu Asp Leu Arg His Ser Leu Met
 225 230 235 240
 Pro Met Leu Glu Thr Leu Lys Thr Lys Ala Gln Ser Val Ile Asp Lys
 245 250 255
 Ala Ser Glu Thr Leu Thr Ala Gln
 260
 <210> 23
 <211> 259
 <212> PRT
 <213> Rattus norvegicus
 <400> 23
 Met Lys Ala Ala Val Leu Ala Val Ala Leu Val Phe Leu Thr Gly Cys
 1 5 10 15
 Gln Ala Trp Glu Phe Trp Gln Gln Asp Glu Pro Gln Ser Gln Trp Asp
 20 25 30
 Arg Val Lys Asp Phe Ala Thr Val Tyr Val Asp Ala Val Lys Asp Ser
 35 40 45
 Gly Arg Asp Tyr Val Ser Gln Phe Glu Ser Ser Thr Leu Gly Lys Gln
 50 55 60
 Leu Asn Leu Asn Leu Leu Asp Asn Trp Asp Thr Leu Gly Ser Thr Val
 65 70 75 80
 Gly Arg Leu Gln Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Ala
 85 90 95
 Asn Leu Glu Lys Glu Thr Asp Trp Leu Arg Asn Glu Met Asn Lys Asp
 100 105 110
 Leu Glu Asn Val Lys Gln Lys Met Gln Pro His Leu Asp Glu Phe Gln
 115 120 125
 Glu Lys Trp Asn Glu Glu Val Glu Ala Tyr Arg Gln Lys Leu Glu Pro
 130 135 140

Leu Gly Thr Glu Leu His Lys Asn Ala Lys Glu Met Gln Arg His Leu
 145 150 155 160

Lys Val Val Ala Glu Glu Phe Arg Asp Arg Met Arg Val Asn Ala Asp
 165 170 175

Ala Leu Arg Ala Lys Phe Gly Leu Tyr Ser Asp Gln Met Arg Glu Asn
 180 185 190

Leu Ala Gln Arg Leu Thr Glu Ile Arg Asn His Pro Thr Leu Ile Glu
 195 200 205

Tyr His Thr Lys Ala Gly Asp His Leu Arg Thr Leu Gly Glu Lys Ala
 210 215 220

Lys Pro Ala Leu Asp Asp Leu Gly Gln Gly Leu Met Pro Val Leu Glu
 225 230 235 240

Ala Trp Lys Ala Lys Ile Met Ser Met Ile Asp Glu Ala Lys Lys Lys
 245 250 255

Leu Asn Ala

<210> 24
 <211> 241
 <212> PRT
 <213> Erinaceus europaeus

<400> 24

Asp Glu Ala Lys Ser Tyr Trp Asp Gln Ile Lys Asp Met Leu Thr Val
 1 5 10 15

Tyr Val Asp Thr Ala Lys Asp Ser Gly Lys Asp Tyr Leu Thr Ser Leu
 20 25 30

Asp Thr Ser Ala Leu Gly Gln Gln Leu Asn Lys Lys Leu Ala Asp Asn
 35 40 45

Trp Asp Thr Val Ser Ser Ala Leu Leu Lys Ala Arg Glu Gln Met Lys
 50 55 60

Pro Ile Ala Met Glu Phe Trp Gly Asn Leu Glu Lys Asp Thr Glu Gly
 65 70 75 80

Leu Arg Gln Thr Val Ser Lys Asp Leu Glu Leu Val Lys Glu Lys Val
85 90 95

Gln Pro Tyr Leu Asp Ser Phe Gln Lys Lys Val Glu Glu Glu Leu Glu
100 105 110

Leu Tyr Arg Gln Lys Val Ala Pro Leu Ser Ala Glu Trp Arg Glu Gln
115 120 125

Ala Arg Gln Lys Ala Gln Glu Leu Gln Gln Lys Ala Gly Glu Leu Gly
130 135 140

Gln Gln His Arg Asp Arg Val Arg Thr His Val Asp Ala Leu Arg Thr
145 150 155 160

Asp Leu Ala Pro Tyr Gly Glu Glu Ala Arg Lys Leu Leu Leu Gln Arg
165 170 175

Leu Gln Asp Ile Lys Ala Lys Ser Gly Asp Leu Ala Glu Tyr Gln Thr
180 185 190

Lys Leu Ser Glu His Leu Lys Ser Phe Gly Glu Lys Ala Gln Pro Thr
195 200 205

Leu Gln Asp Leu Arg His Gly Leu Glu Pro Leu Trp Glu Gly Ile Lys
210 215 220

Ala Gly Ala Met Ser Met Leu Glu Glu Leu Gly Lys Lys Leu Asn Ser
225 230 235 240

Gln

<210> 25

<211> 264

<212> PRT

<213> Gallus gallus

<400> 25

Met Arg Gly Val Leu Val Thr Leu Ala Val Leu Phe Leu Thr Gly Thr
1 5 10 15

Gln Ala Arg Ser Phe Trp Gln His Asp Glu Pro Gln Thr Pro Leu Asp
20 25 30

Arg Ile Arg Asp Met Val Asp Val Tyr Leu Glu Thr Val Lys Ala Ser
 35 40 45
 Gly Lys Asp Ala Ile Ala Gln Phe Glu Ser Ser Ala Val Gly Lys Gln
 50 55 60
 Leu Asp Leu Lys Leu Ala Asp Asn Leu Asp Thr Leu Ser Ala Ala Ala
 65 70 75 80
 Ala Lys Leu Arg Glu Asp Met Ala Pro Tyr Tyr Lys Glu Val Arg Glu
 85 90 95
 Met Trp Leu Lys Asp Thr Glu Ala Leu Arg Ala Glu Leu Thr Lys Asp
 100 105 110
 Leu Glu Glu Val Lys Glu Lys Ile Arg Pro Phe Leu Asp Gln Phe Ser
 115 120 125
 Ala Lys Trp Thr Glu Glu Leu Glu Gln Tyr Arg Gln Arg Leu Thr Pro
 130 135 140
 Val Ala Gln Glu Leu Lys Glu Leu Thr Lys Gln Lys Val Glu Leu Met
 145 150 155 160
 Gln Ala Lys Leu Thr Pro Val Ala Glu Glu Ala Arg Asp Arg Leu Arg
 165 170 175
 Gly His Val Glu Glu Leu Arg Lys Asn Leu Ala Pro Tyr Ser Asp Glu
 180 185 190
 Leu Arg Gln Lys Leu Ser Gln Lys Leu Glu Glu Ile Arg Glu Lys Gly
 195 200 205
 Ile Pro Gln Ala Ser Glu Tyr Gln Ala Lys Val Met Glu Gln Leu Ser
 210 215 220
 Asn Leu Arg Glu Lys Met Thr Pro Leu Val Gln Glu Phe Arg Glu Arg
 225 230 235 240
 Leu Thr Pro Tyr Ala Glu Asn Leu Lys Asn Arg Leu Ile Ser Phe Leu
 245 250 255

Asp Glu Leu Gln Lys Ser Val Ala
260

<210> 26
<211> 264
<212> PRT
<213> Coturnix coturnix japonica

<400> 26

Met Arg Gly Val Leu Val Thr Leu Ala Val Leu Phe Leu Thr Gly Thr
1 5 10 15

Gln Ala Arg Ser Phe Trp Gln His Asp Asp Pro Gln Thr Pro Leu Asp
20 25 30

Arg Ile Arg Asp Met Leu Asp Val Tyr Leu Glu Thr Val Lys Ala Ser
35 40 45

Gly Lys Asp Ala Ile Ser Gln Phe Glu Ser Ser Ala Val Gly Lys Gln
50 55 60

Leu Asp Leu Lys Leu Ala Asp Asn Leu Asp Thr Leu Ser Ala Ala Ala
65 70 75 80

Ala Lys Leu Arg Glu Asp Met Thr Pro Tyr Tyr Arg Glu Val Arg Glu
85 90 95

Met Trp Leu Lys Asp Thr Glu Ala Leu Arg Ala Glu Leu Thr Lys Asp
100 105 110

Leu Glu Glu Val Lys Glu Lys Ile Arg Pro Phe Leu Asp Gln Phe Ser
115 120 125

Ala Lys Trp Thr Glu Glu Val Glu Gln Tyr Arg Gln Arg Leu Ala Pro
130 135 140

Val Ala Gln Glu Leu Lys Asp Leu Thr Lys Gln Lys Val Glu Leu Met
145 150 155 160

Gln Ala Lys Leu Thr Pro Val Ala Glu Glu Val Arg Asp Arg Leu Arg
165 170 175

Glu Gln Val Glu Glu Leu Arg Lys Asn Leu Ala Pro Tyr Ser Ser Glu
180 185 190

Leu Arg Gln Lys Leu Ser Gln Lys Leu Glu Glu Ile Arg Glu Arg Gly
 195 200 205

Ile Pro Gln Ala Ser Glu Tyr Gln Ala Lys Val Val Glu Gln Leu Ser
 210 215 220

Asn Leu Arg Glu Lys Met Thr Pro Leu Val Gln Glu Phe Lys Glu Arg
 225 230 235 240

Leu Thr Pro Tyr Ala Glu Asn Leu Lys Asn Arg Leu Ile Asp Leu Leu
 245 250 255

Asp Glu Val Gln Lys Thr Met Ala
 260

<210> 27
 <211> 264
 <212> PRT
 <213> Anas platyrhynchos

<400> 27

Met Arg Val Val Val Val Thr Leu Ala Leu Leu Phe Leu Thr Gly Thr
 1 5 10 15

Gln Ala Arg Tyr Phe Trp Gln His Asp Glu Pro Gln Ala Pro Leu Asp
 20 25 30

Arg Leu Arg Asp Leu Val Asp Val Tyr Leu Glu Thr Val Lys Ala Ser
 35 40 45

Gly Lys Asp Ala Ile Ala Gln Phe Glu Ala Ser Ala Val Gly Lys Gln
 50 55 60

Leu Asp Leu Lys Leu Ala Asp Asn Leu Asp Thr Leu Gly Ala Ala Ala
 65 70 75 80

Ala Lys Leu Arg Glu Asp Met Ala Pro Tyr Tyr Lys Glu Val Arg Glu
 85 90 95

Met Trp Leu Lys Asp Thr Glu Ser Leu Arg Ala Glu Leu Thr Lys Asp
 100 105 110

Leu Glu Glu Val Lys Glu Lys Ile Arg Pro Phe Leu Asp Gln Phe Ser
 115 120 125

Ala Lys Trp Thr Glu Glu Leu Glu Gln Tyr Arg Gln Arg Leu Ala Pro
 130 135 140

Val Ala Glu Glu Leu Lys Glu Leu Thr Lys Gln Lys Val Glu Leu Met
 145 150 155 160

Gln Gln Lys Leu Thr Pro Val Ala Glu Glu Ala Arg Asp Arg Leu Arg
 165 170 175

Gly His Val Glu Glu Leu Arg Lys Asn Leu Ala Pro Tyr Ser Asp Glu
 180 185 190

Leu Arg Gln Lys Leu Ser Gln Lys Leu Glu Glu Ile Arg Glu Lys Gly
 195 200 205

Ile Pro Gln Ala Ala Glu Tyr Gln Ala Lys Val Val Glu Gln Leu Ser
 210 215 220

Asn Leu Arg Glu Lys Met Thr Pro Leu Val Gln Asp Phe Lys Glu Arg
 225 230 235 240

Leu Thr Pro Tyr Ala Glu Asn Leu Lys Thr Arg Phe Ile Ser Leu Leu
 245 250 255

Asp Glu Leu Gln Lys Thr Val Ala
 260

<210> 28

<211> 262

<212> PRT

<213> Oncorhynchus mykiss

<400> 28

Met Lys Phe Leu Ala Leu Ala Leu Thr Ile Leu Leu Ala Ala Gly Thr
 1 5 10 15

Gln Ala Phe Pro Met Gln Ala Asp Ala Pro Ser Gln Leu Glu His Val
 20 25 30

Lys Ala Ala Leu Ser Met Tyr Ile Ala Gln Val Lys Leu Thr Ala Gln
 35 40 45

Arg Ser Ile Asp Leu Leu Asp Asp Thr Glu Tyr Lys Glu Tyr Lys Met

50		55		60
Gln Leu Thr Gln Ser Leu Asp Asn Leu Gln Gln Tyr Ala Asp Ala Thr				
65		70		75 80
Ser Gln Ser Leu Ala Pro Tyr Ser Glu Ala Phe Gly Thr Gln Leu Thr				
	85		90	95
Asp Ala Thr Ala Ala Val Arg Ala Glu Val Met Lys Asp Val Glu Glu				
	100		105	110
Leu Arg Ser Gln Leu Glu Pro Lys Arg Ala Glu Leu Lys Glu Val Leu				
	115		120	125
Asp Lys His Ile Asp Glu Tyr Arg Lys Lys Leu Glu Pro Leu Ile Lys				
	130		135	140
Glu His Ile Glu Leu Arg Arg Thr Glu Met Glu Ala Phe Arg Ala Lys				
145		150		155 160
Met Glu Pro Ile Val Glu Glu Leu Arg Ala Lys Val Ala Ile Asn Val				
	165		170	175
Glu Glu Thr Lys Thr Lys Leu Met Pro Ile Val Glu Ile Val Arg Ala				
	180		185	190
Lys Leu Thr Glu Arg Leu Glu Glu Leu Arg Thr Leu Ala Ala Pro Tyr				
	195		200	205
Ala Glu Glu Tyr Lys Glu Gln Met Ile Lys Ala Val Gly Glu Val Arg				
	210		215	220
Glu Lys Val Ser Pro Leu Ser Glu Asp Phe Lys Gly Gln Val Gly Pro				
225		230		235 240
Ala Ala Glu Gln Ala Lys Gln Lys Leu Leu Ala Phe Tyr Glu Thr Ile				
	245		250	255
Ser Gln Ala Met Lys Ala				
	260			

<210> 29
 <211> 262
 <212> PRT

<213> Salmo trutta

<400> 29

Met Lys Phe Leu Ala Leu Ala Leu Thr Ile Leu Leu Ala Ala Ala Thr
1 5 10 15

Gln Ala Val Pro Met Gln Ala Asp Ala Pro Ser Gln Leu Glu His Val
20 25 30

Lys Val Ala Met Met Glu Tyr Met Ala Gln Val Lys Glu Thr Gly Gln
35 40 45

Arg Ser Ile Asp Leu Leu Asp Asp Thr Glu Phe Lys Glu Tyr Lys Val
50 55 60

Gln Leu Ser Gln Ser Leu Asp Asn Leu Gln Gln Tyr Ala Gln Thr Thr
65 70 75 80

Ser Gln Ser Leu Ala Pro Tyr Ser Glu Ala Phe Gly Ala Gln Leu Thr
85 90 95

Asp Ala Ala Ala Ala Val Arg Ala Glu Val Met Lys Asp Val Glu Asp
100 105 110

Val Arg Thr Gln Leu Glu Pro Lys Arg Ala Glu Leu Lys Glu Val Leu
115 120 125

Asp Lys His Ile Asp Glu Tyr Arg Lys Lys Leu Glu Pro Leu Ile Lys
130 135 140

Glu Ile Val Glu Gln Arg Arg Thr Glu Leu Glu Ala Phe Arg Val Lys
145 150 155 160

Met Glu Pro Val Val Glu Glu Met Arg Ala Lys Val Ser Thr Asn Val
165 170 175

Glu Glu Thr Lys Ala Lys Leu Met Pro Ile Val Glu Thr Val Arg Ala
180 185 190

Lys Leu Thr Glu Arg Leu Glu Glu Leu Arg Thr Leu Ala Ala Pro Tyr
195 200 205

Ala Glu Glu Tyr Lys Glu Gln Met Phe Lys Ala Val Gly Glu Val Arg
210 215 220

Glu Lys Val Gly Pro Leu Thr Asn Asp Phe Lys Gly Gln Val Gly Pro
 225 230 235 240

Ala Ala Glu Gln Ala Lys Glu Lys Leu Met Asp Phe Tyr Glu Thr Ile
 245 250 255

Ser Gln Ala Met Lys Ala
 260

<210> 30
 <211> 258
 <212> PRT
 <213> Salmo salar

<400> 30

Met Lys Phe Leu Val Leu Ala Leu Thr Ile Leu Leu Ala Ala Gly Thr
 1 5 10 15

Gln Ala Phe Pro Met Gln Ala Asp Ala Pro Ser Gln Leu Glu His Val
 20 25 30

Lys Ala Ala Leu Asn Met Tyr Ile Ala Gln Val Lys Leu Thr Ala Gln
 35 40 45

Arg Ser Ile Asp Leu Leu Asp Asp Thr Glu Tyr Lys Glu Tyr Lys Met
 50 55 60

Gln Leu Ser Gln Ser Leu Asp Asn Leu Gln Gln Phe Ala Asp Ser Thr
 65 70 75 80

Ser Lys Ser Trp Pro Pro Thr Pro Arg Ser Ser Ala Pro Ser Cys Asp
 85 90 95

Ala Thr Ala Thr Val Arg Ala Glu Val Met Lys Asp Val Glu Asp Val
 100 105 110

Arg Thr Gln Leu Glu Pro Lys Arg Ala Glu Leu Thr Glu Val Leu Asn
 115 120 125

Lys His Ile Asp Glu Tyr Arg Lys Lys Leu Glu Pro Leu Ile Lys Gln
 130 135 140

His Ile Glu Leu Arg Arg Thr Glu Met Asp Ala Phe Arg Ala Lys Ile

145 150 155 160
 Asp Pro Val Val Glu Glu Met Arg Ala Lys Val Ala Val Asn Val Glu
 165 170 175
 Glu Thr Lys Thr Lys Leu Met Pro Ile Val Glu Ile Val Arg Ala Lys
 180 185 190
 Leu Thr Glu Arg Leu Glu Glu Leu Arg Thr Leu Ala Ala Pro Tyr Ala
 195 200 205
 Glu Glu Tyr Lys Glu Gln Met Phe Lys Ala Val Gly Glu Val Arg Glu
 210 215 220
 Lys Val Ala Pro Leu Ser Glu Asp Phe Lys Ala Arg Trp Ala Pro Pro
 225 230 235 240
 Pro Arg Arg Pro Ser Lys Ser Ser Trp Leu Ser Thr Arg Pro Ser Ala
 245 250 255

Arg Pro

<210> 31
 <211> 262
 <212> PRT
 <213> Brachydanio rerio

<400> 31

Met Lys Phe Val Ala Leu Ala Leu Thr Leu Leu Leu Ala Leu Gly Ser
 1 5 10 15
 Gln Ala Asn Leu Phe Gln Ala Asp Ala Pro Thr Gln Leu Glu His Tyr
 20 25 30
 Lys Ala Ala Ala Leu Val Tyr Leu Asn Gln Val Lys Asp Gln Ala Glu
 35 40 45
 Lys Ala Leu Asp Asn Leu Asp Gly Thr Asp Tyr Glu Gln Tyr Lys Leu
 50 55 60
 Gln Leu Ser Glu Ser Leu Thr Lys Leu Gln Glu Tyr Ala Gln Thr Thr
 65 70 75 80

Ser Gln Ala Leu Thr Pro Tyr Ala Glu Thr Ile Ser Thr Gln Leu Met
 85 90 95

Glu Asn Thr Lys Gln Leu Arg Glu Arg Val Met Thr Asp Val Glu Asp
 100 105 110

Leu Arg Ser Lys Leu Glu Pro His Arg Ala Glu Leu Tyr Thr Ala Leu
 115 120 125

Gln Lys His Ile Asp Glu Tyr Arg Glu Lys Leu Glu Pro Val Phe Gln
 130 135 140

Glu Tyr Ser Ala Leu Asn Arg Gln Asn Ala Glu Gln Leu Arg Ala Lys
 145 150 155 160

Leu Glu Pro Leu Met Asp Asp Ile Arg Lys Ala Phe Glu Ser Asn Ile
 165 170 175

Glu Glu Thr Lys Ser Lys Val Val Pro Met Val Glu Ala Val Arg Thr
 180 185 190

Lys Leu Thr Glu Arg Leu Glu Asp Leu Arg Thr Met Ala Ala Pro Tyr
 195 200 205

Ala Glu Glu Tyr Lys Glu Gln Leu Val Lys Ala Val Glu Glu Ala Arg
 210 215 220

Glu Lys Ile Ala Pro His Thr Gln Asp Leu Gln Thr Arg Met Glu Pro
 225 230 235 240

Tyr Met Glu Asn Val Arg Thr Thr Phe Ala Gln Met Tyr Glu Thr Ile
 245 250 255

Ala Lys Ala Ile Gln Ala
 260

<210> 32

<211> 260

<212> PRT

<213> Sparus aurata

<400> 32 .

Met Lys Phe Ala Ala Leu Ala Leu Ala Leu Leu Leu Ala Val Gly Ser
 1 5 10 15

His Ala Ala Ser Met Gln Ala Asp Ala Pro Ser Gln Leu Asp His Ala
 20 25 30

Arg Ala Val Leu Asp Val Tyr Leu Thr Gln Val Lys Asp Met Ser Leu
 35 40 45

Arg Ala Val Asn Gln Leu Asp Asp Pro Gln Tyr Ala Glu Phe Lys Thr
 50 55 60

Asn Leu Ala Gln Arg Ile Glu Glu Met Tyr Thr Gln Ile Lys Thr Leu
 65 70 75 80

Gln Gly Ser Val Ser Pro Met Thr Asp Ser Phe Tyr Asn Thr Val Met
 85 90 95

Glu Val Thr Lys Asp Thr Arg Glu Ser Leu Asn Val Asp Leu Glu Ala
 100 105 110

Leu Lys Ser Ser Leu Ala Pro Gln Asn Glu Gln Leu Lys Gln Val Ile
 115 120 125

Glu Lys His Leu Asn Asp Tyr Arg Thr Leu Leu Thr Pro Ile Tyr Asn
 130 135 140

Asp Tyr Lys Thr Lys His Asp Glu Glu Met Ala Ala Leu Lys Thr Arg
 145 150 155 160

Leu Glu Pro Val Met Glu Glu Leu Arg Thr Lys Ile Gln Ala Asn Val
 165 170 175

Glu Glu Thr Lys Ala Val Leu Met Pro Met Val Glu Thr Val Arg Thr
 180 185 190

Lys Val Thr Glu Arg Leu Glu Ser Leu Arg Glu Val Val Gln Pro Tyr
 195 200 205

Val Gln Glu Tyr Lys Glu Gln Met Lys Gln Met Tyr Asp Gln Ala Gln
 210 215 220

Thr Val Asp Thr Asp Ala Leu Arg Thr Lys Ile Thr Pro Leu Val Glu
 225 230 235 240

Glu Ile Lys Val Lys Met Asn Ala Ile Phe Glu Ile Ile Ala Ala Ser

245

250

255

Val Thr Lys Ser
260

<210> 33
<211> 396
<212> PRT
<213> Homo sapiens

<400> 33

Met Phe Leu Lys Ala Val Val Leu Thr Leu Ala Leu Val Ala Val Ala
1 5 10 15

Gly Ala Arg Ala Glu Val Ser Ala Asp Gln Val Ala Thr Val Met Trp
20 25 30

Asp Tyr Phe Ser Gln Leu Ser Asn Asn Ala Lys Glu Ala Val Glu His
35 40 45

Leu Gln Lys Ser Glu Leu Thr Gln Gln Leu Asn Ala Leu Phe Gln Asp
50 55 60

Lys Leu Gly Glu Val Asn Thr Tyr Ala Gly Asp Leu Gln Lys Lys Leu
65 70 75 80

Val Pro Phe Ala Thr Glu Leu His Glu Arg Leu Ala Lys Asp Ser Glu
85 90 95

Lys Leu Lys Glu Glu Ile Gly Lys Glu Leu Glu Glu Leu Arg Ala Arg
100 105 110

Leu Leu Pro His Ala Asn Glu Val Ser Gln Lys Ile Gly Asp Asn Leu
115 120 125

Arg Glu Leu Gln Gln Arg Leu Glu Pro Tyr Ala Asp Gln Leu Arg Thr
130 135 140

Gln Val Asn Thr Gln Ala Glu Gln Leu Arg Arg Gln Leu Thr Pro Tyr
145 150 155 160

Ala Gln Arg Met Glu Arg Val Leu Arg Glu Asn Ala Asp Ser Leu Gln
165 170 175

Ala Ser Leu Arg Pro His Ala Asp Glu Leu Lys Ala Lys Ile Asp Gln
 180 185 190

Asn Val Glu Glu Leu Lys Gly Arg Leu Thr Pro Tyr Ala Asp Glu Phe
 195 200 205

Lys Val Lys Ile Asp Gln Thr Val Glu Glu Leu Arg Arg Ser Leu Ala
 210 215 220

Pro Tyr Ala Gln Asp Thr Gln Glu Lys Leu Asn His Gln Leu Glu Gly
 225 230 235 240

Leu Thr Phe Gln Met Lys Lys Asn Ala Glu Glu Leu Lys Ala Arg Ile
 245 250 255

Ser Ala Ser Ala Glu Glu Leu Arg Gln Arg Leu Ala Pro Leu Ala Glu
 260 265 270

Asp Val Arg Gly Asn Leu Lys Gly Asn Thr Glu Gly Leu Gln Lys Ser
 275 280 285

Leu Ala Glu Leu Gly Gly His Leu Asp Gln Gln Val Glu Glu Phe Arg
 290 295 300

Arg Arg Val Glu Pro Tyr Gly Glu Asn Phe Asn Lys Ala Leu Val Gln
 305 310 315 320

Gln Met Glu Gln Leu Arg Gln Lys Leu Gly Pro His Ala Gly Asp Val
 325 330 335

Glu Gly His Leu Ser Phe Leu Glu Lys Asp Leu Arg Asp Lys Val Asn
 340 345 350

Ser Phe Phe Ser Thr Phe Lys Glu Lys Glu Ser Gln Asp Lys Thr Leu
 355 360 365

Ser Leu Pro Glu Leu Glu Gln Gln Gln Glu Gln Gln Gln Glu Gln Gln
 370 375 380

Gln Glu Gln Val Gln Met Leu Ala Pro Leu Glu Ser
 385 390 395

<210> 34
 <211> 429

<212> PRT

<213> *Macaca fascicularis*

<400> 34

Met Phe Leu Lys Ala Val Val Leu Thr Leu Ala Leu Val Ala Val Thr
 1 5 10 15

Gly Ala Arg Ala Glu Val Ser Ala Asp Gln Val Ala Thr Val Met Trp
 20 25 30

Asp Tyr Phe Ser Gln Leu Ser Ser Asn Ala Lys Glu Ala Val Glu His
 35 40 45

Leu Gln Lys Ser Glu Leu Thr Gln Gln Leu Asn Ala Leu Phe Gln Asp
 50 55 60

Lys Leu Gly Glu Val Asn Thr Tyr Ala Gly Asp Leu Gln Lys Lys Leu
 65 70 75 80

Val Pro Phe Ala Thr Glu Leu His Glu Arg Leu Ala Lys Asp Ser Glu
 85 90 95

Lys Leu Lys Glu Glu Ile Arg Lys Glu Leu Glu Glu Val Arg Ala Arg
 100 105 110

Leu Leu Pro His Ala Asn Glu Val Ser Gln Lys Ile Gly Glu Asn Val
 115 120 125

Arg Glu Leu Gln Gln Arg Leu Glu Pro Tyr Thr Asp Gln Leu Arg Thr
 130 135 140

Gln Val Asn Thr Gln Thr Glu Gln Leu Arg Arg Gln Leu Thr Pro Tyr
 145 150 155 160

Ala Gln Arg Met Glu Arg Val Leu Arg Glu Asn Ala Asp Ser Leu Gln
 165 170 175

Thr Ser Leu Arg Pro His Ala Asp Gln Leu Lys Ala Lys Ile Asp Gln
 180 185 190

Asn Val Glu Glu Leu Lys Glu Arg Leu Thr Pro Tyr Ala Asp Glu Phe
 195 200 205

Lys Val Lys Ile Asp Gln Thr Val Glu Glu Leu Arg Arg Ser Leu Ala

210	215	220
Pro Tyr Ala Gln Asp 225	Ala Gln Glu Lys Leu 230	Asn His Gln Leu Glu Gly 235 240
Leu Ala Phe Gln Met 245	Lys Lys Asn Ala Glu Glu 250	Leu Lys Ala Arg Ile 255
Ser Ala Ser Ala Glu Glu 260	Leu Arg Gln Arg Leu Ala 265	Pro Leu Ala Glu 270
Asp Met Arg Gly Asn Leu 275	Arg Gly Asn Thr Glu Gly 280	Leu Gln Lys Ser 285
Leu Ala Glu Leu Gly Gly 290	His Leu Asp Arg His Val 295 300	Glu Glu Phe Arg
Leu Arg Val Glu Pro Tyr 305	Gly Glu Asn Phe Asn Lys 310 315	Ala Leu Val Gln 320
Gln Met Glu Gln Leu Arg 325	Gln Lys Leu Gly Pro His 330	Ala Gly Asp Val 335
Glu Gly His Leu Ser Phe 340	Leu Glu Lys Asp Leu Arg 345	Asp Lys Val Asn 350
Ser Phe Phe Ser Thr Phe 355	Lys Glu Lys Glu Ser Gln 360	Asp Asn Thr Leu 365
Ser Leu Pro Glu Pro Glu 370	Gln Gln Arg Glu Gln Gln 375 380	Gln Glu Gln Gln Gln
Gln Glu Gln Glu Gln Glu 385	Gln Gln Gln Gln Gln Glu 390 395	Gln Gln Gln Gln Gln
Gln Glu Gln Gln Arg Glu 405	Gln Gln Gln Gln Glu Gln 410	Gln Gln Glu Gln 415
Gln Gln Glu Gln Val Gln 420	Met Leu Ala Pro Leu Glu 425	Ser

<210> 35
 <211> 395
 <212> PRT

<213> Mus musculus

<400> 35

Met Phe Leu Lys Ala Ala Val Leu Thr Leu Ala Leu Val Ala Ile Thr
1 5 10 15

Gly Thr Arg Ala Glu Val Thr Ser Asp Gln Val Ala Asn Val Val Trp
20 25 30

Asp Tyr Phe Thr Gln Leu Ser Asn Asn Ala Lys Glu Ala Val Glu Gln
35 40 45

Phe Gln Lys Thr Asp Val Thr Gln Gln Leu Ser Thr Leu Phe Gln Asp
50 55 60

Lys Leu Gly Asp Ala Ser Thr Tyr Ala Asp Gly Val His Asn Lys Leu
65 70 75 80

Val Pro Phe Val Val Gln Leu Ser Gly His Leu Ala Lys Glu Thr Glu
85 90 95

Arg Val Lys Glu Glu Ile Lys Lys Glu Leu Glu Asp Leu Arg Asp Arg
100 105 110

Met Met Pro His Ala Asn Lys Val Thr Gln Thr Phe Gly Glu Asn Met
115 120 125

Gln Lys Leu Gln Glu His Leu Lys Pro Tyr Ala Val Asp Leu Gln Asp
130 135 140

Gln Ile Asn Thr Gln Thr Gln Glu Met Lys Leu Gln Leu Thr Pro Tyr
145 150 155 160

Ile Gln Arg Met Gln Thr Thr Ile Lys Glu Asn Val Asp Asn Leu His
165 170 175

Thr Ser Met Met Pro Leu Ala Thr Asn Leu Lys Asp Lys Phe Asn Arg
180 185 190

Asn Met Glu Glu Leu Lys Gly His Leu Thr Pro Arg Ala Asn Glu Leu
195 200 205

Lys Ala Thr Ile Asp Gln Asn Leu Glu Asp Leu Arg Arg Ser Leu Ala
210 215 220

Pro Leu Thr Val Gly Val Gln Glu Lys Leu Asn His Gln Met Glu Gly
 225 230 235 240

Leu Ala Phe Gln Met Lys Lys Asn Ala Glu Glu Leu Gln Thr Lys Val
 245 250 255

Ser Ala Lys Ile Asp Gln Leu Gln Lys Asn Leu Ala Pro Leu Val Glu
 260 265 270

Asp Val Gln Ser Lys Val Lys Gly Asn Thr Glu Gly Leu Gln Lys Ser
 275 280 285

Leu Glu Asp Leu Asn Arg Gln Leu Glu Gln Gln Val Glu Glu Phe Arg
 290 295 300

Arg Thr Val Glu Pro Met Gly Glu Met Phe Asn Lys Ala Leu Val Gln
 305 310 315 320

Gln Leu Glu Gln Phe Arg Gln Gln Leu Gly Pro Asn Ser Gly Glu Val
 325 330 335

Glu Ser His Leu Ser Phe Leu Glu Lys Ser Leu Arg Glu Lys Val Asn
 340 345 350

Ser Phe Met Ser Thr Leu Glu Lys Lys Gly Ser Pro Asp Gln Pro Gln
 355 360 365

Ala Leu Pro Leu Pro Glu Gln Ala Gln Glu Gln Ala Gln Glu Gln Ala
 370 375 380

Gln Glu Gln Val Gln Pro Lys Pro Leu Glu Ser
 385 390 395

<210> 36
 <211> 401
 <212> PRT
 <213> Papio anubis

<400> 36

Gly Ala Arg Ala Glu Val Ser Ala Asp Gln Val Ala Thr Val Met Trp
 1 5 10 15

Asp Tyr Phe Ser Gln Leu Ser Ser Asn Ala Lys Glu Ala Val Glu His

20

25

30

Leu Gln Lys Ser Glu Leu Thr Gln Gln Leu Asn Ala Leu Phe Gln Asp
 35 40 45

Lys Leu Gly Glu Val Asn Thr Tyr Ala Gly Asp Leu Gln Lys Lys Leu
 50 55 60

Val Pro Phe Ala Thr Glu Leu His Glu Arg Leu Ala Lys Asp Ser Lys
 65 70 75 80

Lys Leu Lys Glu Glu Ile Arg Lys Glu Leu Glu Glu Val Arg Ala Arg
 85 90 95

Leu Leu Pro His Ala Asn Glu Val Ser Gln Lys Ile Gly Glu Asn Val
 100 105 110

Arg Glu Leu Gln Gln Arg Leu Glu Pro Tyr Thr Asp Gln Leu Arg Thr
 115 120 125

Gln Val Asn Thr Gln Thr Glu Gln Leu Arg Arg Gln Leu Thr Pro Tyr
 130 135 140

Ala Gln Arg Met Glu Arg Val Leu Arg Glu Asn Ala Asp Ser Leu Gln
 145 150 155 160

Thr Ser Leu Arg Pro His Ala Asp Gln Leu Lys Ala Lys Ile Asp Gln
 165 170 175

Asn Val Glu Glu Leu Lys Gly Arg Leu Thr Pro Tyr Ala Asp Glu Phe
 180 185 190

Lys Val Lys Ile Asp Gln Thr Val Glu Glu Leu Arg Arg Ser Leu Ala
 195 200 205

Pro Tyr Ala Gln Asp Ala Gln Glu Lys Leu Asn His Gln Leu Glu Gly
 210 215 220

Leu Ala Phe Gln Met Lys Lys Asn Ala Glu Glu Leu Lys Ala Arg Ile
 225 230 235 240

Ser Ala Ser Ala Glu Glu Leu Arg Gln Arg Leu Ala Pro Leu Ala Glu
 245 250 255

Asp Met Arg Gly Asn Leu Arg Gly Asn Thr Glu Gly Leu Gln Lys Ser
 260 265 270

Leu Ala Glu Leu Gly Gly His Leu Asp Arg His Val Glu Glu Phe Arg
 275 280 285

Leu Arg Val Glu Pro Tyr Gly Glu Asn Phe Asn Lys Ala Leu Val Gln
 290 295 300

Gln Met Glu Gln Leu Arg Gln Lys Leu Gly Pro His Ala Gly Asp Val
 305 310 315 320

Glu Gly His Leu Ser Phe Leu Glu Lys Asp Leu Arg Asp Lys Val Asn
 325 330 335

Ser Phe Phe Ser Thr Phe Lys Glu Lys Glu Ser Gln Asp Asn Thr Leu
 340 345 350

Ser Leu Pro Glu Pro Glu Gln Gln Gln Glu Gln Gln Gln Glu Gln Glu
 355 360 365

Gln Gln Gln Glu Gln Gln Glu Glu Gln Gln Gln Gln Glu Gln Gln Gln
 370 375 380

Glu Gln Glu Gln Gln Gln Glu Gln Val Gln Met Leu Ala Pro Leu Glu
 385 390 395 400

Ser

<210> 37
 <211> 382
 <212> PRT
 <213> Sus scrofa

<400> 37

Met Phe Leu Lys Ala Val Val Leu Ser Leu Ala Leu Val Ala Val Thr
 1 5 10 15

Gly Ala Arg Ala Glu Val Asn Ala Asp Gln Val Ala Thr Val Met Trp
 20 25 30

Asp Tyr Phe Ser Gln Leu Gly Ser Asn Ala Lys Lys Ala Val Glu His
 35 40 45

Leu Gln Lys Ser Glu Leu Thr Gln Gln Leu Asn Thr Leu Phe Gln Asp
 50 55 60

Lys Leu Gly Glu Val Asn Thr Tyr Thr Glu Asp Leu Gln Lys Lys Leu
 65 70 75 80

Val Pro Phe Ala Thr Glu Leu His Glu Arg Leu Thr Lys Asp Ser Glu
 85 90 95

Lys Leu Lys Glu Glu Ile Arg Arg Glu Leu Glu Glu Leu Arg Ala Arg
 100 105 110

Leu Leu Pro His Ala Thr Glu Val Ser Gln Lys Ile Gly Asp Asn Val
 115 120 125

Arg Glu Leu Gln Gln Arg Leu Gly Pro Phe Thr Gly Gly Leu Arg Thr
 130 135 140

Gln Val Asn Thr Gln Val Gln Gln Leu Gln Arg Gln Leu Lys Pro Tyr
 145 150 155 160

Ala Glu Arg Met Glu Ser Val Leu Arg Gln Asn Ile Arg Asn Leu Glu
 165 170 175

Ala Ser Val Ala Pro Tyr Ala Asp Glu Phe Lys Ala Lys Ile Asp Gln
 180 185 190

Asn Val Glu Glu Leu Lys Gly Ser Leu Thr Pro Tyr Ala Glu Glu Leu
 195 200 205

Lys Ala Lys Ile Asp Gln Asn Val Glu Glu Leu Arg Arg Ser Leu Ala
 210 215 220

Pro Tyr Ala Gln Asp Val Gln Glu Lys Leu Asn His Gln Leu Glu Gly
 225 230 235 240

Leu Ala Phe Gln Met Lys Lys Gln Ala Glu Glu Leu Lys Ala Lys Ile
 245 250 255

Ser Ala Asn Ala Asp Glu Leu Arg Gln Lys Leu Val Pro Val Ala Glu
 260 265 270

Asn Val His Gly His Leu Lys Gly Asn Thr Glu Gly Leu Gln Lys Ser
 275 280 285

Leu Leu Glu Leu Arg Ser His Leu Asp Gln Gln Val Glu Glu Phe Arg
 290 295 300

Leu Lys Val Glu Pro Tyr Gly Glu Thr Phe Asn Lys Ala Leu Val Gln
 305 310 315 320

Gln Val Glu Asp Leu Arg Gln Lys Leu Gly Pro Leu Ala Gly Asp Val
 325 330 335

Glu Gly His Leu Ser Phe Leu Glu Lys Asp Leu Arg Asp Lys Val Asn
 340 345 350

Thr Phe Phe Ser Thr Leu Lys Glu Glu Ala Ser Gln Gly Gln Ser Gln
 355 360 365

Ala Leu Pro Ala Gln Glu Lys Ala Gln Ala Pro Leu Glu Gly
 370 375 380

<210> 38

<211> 391

<212> PRT

<213> Rattus norvegicus

<400> 38

Met Phe Leu Lys Ala Val Val Leu Thr Val Ala Leu Val Ala Ile Thr
 1 5 10 15

Gly Thr Gln Ala Glu Val Thr Ser Asp Gln Val Ala Asn Val Met Trp
 20 25 30

Asp Tyr Phe Thr Gln Leu Ser Asn Asn Ala Lys Glu Ala Val Glu Gln
 35 40 45

Leu Gln Lys Thr Asp Val Thr Gln Gln Leu Asn Thr Leu Phe Gln Asp
 50 55 60

Lys Leu Gly Asn Ile Asn Thr Tyr Ala Asp Asp Leu Gln Asn Lys Leu
 65 70 75 80

Val Pro Phe Ala Val Gln Leu Ser Gly His Leu Thr Lys Glu Thr Glu
 85 90 95

Arg Val Arg Glu Glu Ile Gln Lys Glu Leu Glu Asp Leu Arg Ala Asn
 100 105 110

Met Met Pro His Ala Asn Lys Val Ser Gln Met Phe Gly Asp Asn Val
 115 120 125

Gln Lys Leu Gln Glu His Leu Arg Pro Tyr Ala Thr Asp Leu Gln Ala
 130 135 140

Gln Ile Asn Ala Gln Thr Gln Asp Met Lys Arg Gln Leu Thr Pro Tyr
 145 150 155 160

Ile Gln Arg Met Gln Thr Thr Ile Gln Asp Asn Val Glu Asn Leu Gln
 165 170 175

Ser Ser Met Val Pro Phe Ala Asn Glu Leu Lys Glu Lys Phe Asn Gln
 180 185 190

Asn Met Glu Gly Leu Lys Gly Gln Leu Thr Pro Arg Ala Asn Glu Leu
 195 200 205

Lys Ala Thr Ile Asp Gln Asn Leu Glu Asp Leu Arg Ser Arg Leu Ala
 210 215 220

Pro Leu Ala Glu Gly Val Gln Glu Lys Leu Asn His Gln Met Glu Gly
 225 230 235 240

Leu Ala Phe Gln Met Lys Lys Asn Ala Glu Glu Leu Gln Thr Lys Val
 245 250 255

Ser Thr Asn Ile Asp Gln Leu Gln Lys Asn Leu Ala Pro Leu Val Glu
 260 265 270

Asp Val Gln Ser Lys Leu Lys Gly Asn Thr Glu Gly Leu Gln Lys Ser
 275 280 285

Leu Glu Asp Leu Asn Lys Gln Leu Asp Gln Gln Val Glu Val Phe Arg
 290 295 300

Arg Ala Val Glu Pro Leu Gly Asp Lys Phe Asn Met Ala Leu Val Gln
 305 310 315 320

Gln Met Glu Lys Phe Arg Gln Gln Leu Gly Ser Asp Ser Gly Asp Val

325 330 335
 Glu Ser His Leu Ser Phe Leu Glu Lys Asn Leu Arg Glu Lys Val Ser
 340 345 350
 Ser Phe Met Ser Thr Leu Gln Lys Lys Gly Ser Pro Asp Gln Pro Leu
 355 360 365
 Ala Leu Pro Leu Pro Glu Gln Val Gln Glu Gln Val Gln Glu Gln Val
 370 375 380
 Gln Pro Lys Pro Leu Glu Ser
 385 390

<210> 39
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 39

Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
 1 5 10 15

Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
 20 25 30

Val Cys Leu Lys
 35

<210> 40
 <211> 36
 <212> PRT
 <213> Mus musculus

<400> 40

Leu Val Ser Ser Lys Met Phe Glu Glu Leu Lys Asn Arg Met Asp Val
 1 5 10 15

Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Lys Gln Ala Leu Gln Thr
 20 25 30

Val Cys Leu Lys
 35

<210> 41

<211> 36
 <212> PRT
 <213> Box taurus

<400> 41

Arg Arg Val Lys Glu Lys Asp Gly Asp Leu Lys Thr Gln Val Glu Lys
 1 5 10 15

Leu Trp Arg Glu Val Asn Ala Leu Lys Glu Met Gln Ala Leu Gln Thr
 20 25 30

Val Cys Leu Arg
 35

<210> 42
 <211> 36
 <212> PRT
 <213> Carcharhinus springeri

<400> 42

Ser Lys Ser Gly Lys Gly Lys Asp Asp Leu Arg Asn Glu Ile Asp Lys
 1 5 10 15

Leu Trp Arg Glu Val Asn Ser Leu Lys Glu Met Gln Ala Leu Gln Thr
 20 25 30

Val Cys Leu Lys
 35

<210> 43
 <211> 1282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7 H6UbiFx Apo A-1 plasmid

<220>
 <221> CDS
 <222> (100)..(1107)
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<400> 43
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 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5

cat cac cat cac gga tca cag atc ttt gtg aag acc ctc act ggc aaa His His His His Gly Ser Gln Ile Phe Val Lys Thr Leu Thr Gly Lys 10 15 20	162
acc atc acc ctt gag gtc gag ccc agt gac acc att gag aat gtc aaa Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys 25 30 35	210
gcc aaa att caa gac aag gag ggt atc cca cct gac cag cag cgt ctg Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu 40 45 50	258
ata ttt gcc ggc aaa cag ctg gaa gat gga cgt act ttg tct gac tac Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr 55 60 65	306
aat att caa aag gag tct act ctt cat ctt gtg ttg aga ctt cgt ggt Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly 70 75 80 85	354
gga tcc atc gag ggt agg ggt gga gat gaa ccc ccc cag agc ccc tgg Gly Ser Ile Glu Gly Arg Gly Gly Asp Glu Pro Pro Gln Ser Pro Trp 90 95 100	402
gat cga gtg aag gac ctg gcc act gtg tac gtg gat gtg ctc aaa gac Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp 105 110 115	450
agc ggc aga gac tat gtg tcc cag ttt gaa ggc tcc gcc ttg gga aaa Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys 120 125 130	498
cag cta aac cta aag ctc ctt gac aac tgg gac agc gtg acc tcc acc Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr 135 140 145	546
ttc agc aag ctg cgc gaa cag ctc ggc cct gtg acc cag gag ttc tgg Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp 150 155 160 165	594
gat aac ctg gaa aag gag aca gag ggc ctg agg cag gag atg agc aag Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys 170 175 180	642
gat ctg gag gag gtg aag gcc aag gtg cag ccc tac ctg gac gac ttc Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe 185 190 195	690
cag aag aag tgg cag gag gag atg gag ctc tac cgc cag aag gtg gag Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu 200 205 210	738
ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag aag ctg cac gag Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu 215 220 225	786
ctg caa gag aag ctg agc cca ctg ggc gag gag atg cgc gac cgc gcg Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala	834

230	235	240	245	
cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc ccc tac agc gac				882
Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp				
	250	255	260	
gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct ctc aag gag aac				930
Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn				
	265	270	275	
ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc acc gag cat ctg				978
Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu				
	280	285	290	
agc acg ctc agc gag aag gcc aag ccc gcg ctc gag gac ctc cgc caa				1026
Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln				
	295	300	305	
ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc ttc ctg agc gct				1074
Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala				
	310	315	320	325
ctc gag gag tac act aag aag ctc aac acc cag taagcatgca agcttgaatt				1127
Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln				
	330	335		
ccgatccggc tgctaacaaa gcccgaaagg aagctgagtt ggctgcctgc caccgctgag				1187
ctgagcaata actagcataa cccctctgcc accgctgtgg ggctctctaaa cgggtcttga				1247
gggggtttttt gctgaaagga ggaactatat ccgat				1282
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<212>	PRT			
<213>	Artificial Sequence			
<220>				
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<400>	44			
Met Gly Ser His His His His His His Gly Ser Gln Ile Phe Val Lys				
1	5	10	15	
Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr				
	20	25	30	
Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro				
	35	40	45	
Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg				
	50	55	60	

Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val
65 70 75 80

Leu Arg Leu Arg Gly Gly Ser Ile Glu Gly Arg Gly Gly Asp Glu Pro
85 90 95

Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val
100 105 110

Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly
115 120 125

Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp
130 135 140

Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val
145 150 155 160

Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg
165 170 175

Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro
180 185 190

Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr
195 200 205

Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg
210 215 220

Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu
225 230 235 240

Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu
245 250 255

Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu
260 265 270

Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys
275 280 285

Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu

290	295	300	
Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val			
305	310	315	320
Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln			
	325	330	335

<210> 45
 <211> 1285
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> T7 H6UbiFx Cys-Apo A-1 plasmid

<220>
 <221> CDS
 <222> (100)..(1110)
 <223>

<400> 45
 gatctcgatc ccgcgaaatt aatacgatac actataggga gaccacaacg gtttcctct 60
 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5
 cat cac cat cac gga tca cag atc ttt gtg aag acc ctc act ggc aaa 162
 His His His His Gly Ser Gln Ile Phe Val Lys Thr Leu Thr Gly Lys
 10 15 20
 acc atc acc ctt gag gtc gag ccc agt gac acc att gag aat gtc aaa 210
 Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys
 25 30 35
 gcc aaa att caa gac aag gag ggt atc cca cct gac cag cag cgt ctg 258
 Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu
 40 45 50
 ata ttt gcc ggc aaa cag ctg gaa gat gga cgt act ttg tct gac tac 306
 Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr
 55 60 65
 aat att caa aag gag tct act ctt cat ctt gtg ttg aga ctt cgt ggt 354
 Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly
 70 75 80 85
 gga tcc atc gag ggt agg ggt gga tgt gat gaa ccc ccc cag agc ccc 402
 Gly Ser Ile Glu Gly Arg Gly Gly Cys Asp Glu Pro Pro Gln Ser Pro
 90 95 100
 tgg gat cga gtg aag gac ctg gcc act gtg tac gtg gat gtg ctc aaa 450
 Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys

105	110	115	
gac agc ggc aga gac tat gtg tcc cag ttt gaa ggc tcc gcc ttg gga Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly 120 125 130			498
aaa cag cta aac cta aag ctc ctt gac aac tgg gac agc gtg acc tcc Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser 135 140 145			546
acc ttc agc aag ctg cgc gaa cag ctc ggc cct gtg acc cag gag ttc Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe 150 155 160 165			594
tgg gat aac ctg gaa aag gag aca gag ggc ctg agg cag gag atg agc Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser 170 175 180			642
aag gat ctg gag gag gtg aag gcc aag gtg cag ccc tac ctg gac gac Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp 185 190 195			690
ttc cag aag aag tgg cag gag gag atg gag ctc tac cgc cag aag gtg Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val 200 205 210			738
gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag aag ctg cac Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His 215 220 225			786
gag ctg caa gag aag ctg agc cca ctg ggc gag gag atg cgc gac cgc Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg 230 235 240 245			834
gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc ccc tac agc Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser 250 255 260			882
gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct ctc aag gag Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu 265 270 275			930
aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc acc gag cat Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His 280 285 290			978
ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc gag gac ctc cgc Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg 295 300 305			1026
caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc ttc ctg agc Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser 310 315 320 325			1074
gct ctc gag gag tac act aag aag ctc aac acc cag taagcatgca Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln 330 335			1120


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agcttgaatt ccgatccggc tgctaacaaa gcccgaaagg aagctgagtt ggctgcctgc 1180
caccgctgag ctgagcaata actagcataa cccctctgcc accgctgtgg ggctctctaaa 1240
cgggtcttga ggggtttttt gctgaaagga ggaactatat ccgat 1285

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<210> 46
<211> 337
<212> PRT
<213> Artificial Sequence

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<220>
<223> T7 H6UbiFx Cys-Apo A-1 plasmid

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<400> 46

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Met Gly Ser His His His His His His Gly Ser Gln Ile Phe Val Lys
1          5          10          15

```

```

Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr
          20          25          30

```

```

Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro
          35          40          45

```

```

Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg
          50          55          60

```

```

Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val
65          70          75          80

```

```

Leu Arg Leu Arg Gly Gly Ser Ile Glu Gly Arg Gly Gly Cys Asp Glu
          85          90          95

```

```

Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr
          100          105          110

```

```

Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu
          115          120          125

```

```

Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp
          130          135          140

```

```

Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro
145          150          155          160

```

```

Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu

```

				165				170				175			
Arg	Gln	Glu	Met 180	Ser	Lys	Asp	Leu	Glu 185	Glu	Val	Lys	Ala	Lys 190	Val	Gln
Pro	Tyr	Leu 195	Asp	Asp	Phe	Gln	Lys 200	Lys	Trp	Gln	Glu	Glu 205	Met	Glu	Leu
Tyr	Arg 210	Gln	Lys	Val	Glu	Pro 215	Leu	Arg	Ala	Glu	Leu 220	Gln	Glu	Gly	Ala
Arg 225	Gln	Lys	Leu	His 230	Glu	Leu	Gln	Glu	Lys	Leu 235	Ser	Pro	Leu	Gly	Glu 240
Glu	Met	Arg	Asp	Arg 245	Ala	Arg	Ala	His	Val 250	Asp	Ala	Leu	Arg	Thr 255	His
Leu	Ala	Pro 260	Tyr	Ser	Asp	Glu	Leu	Arg 265	Gln	Arg	Leu	Ala	Ala 270	Arg	Leu
Glu	Ala	Leu 275	Lys	Glu	Asn	Gly	Gly 280	Ala	Arg	Leu	Ala	Glu 285	Tyr	His	Ala
Lys	Ala 290	Thr	Glu	His	Leu	Ser 295	Thr	Leu	Ser	Glu	Lys 300	Ala	Lys	Pro	Ala
Leu 305	Glu	Asp	Leu	Arg	Gln 310	Gly	Leu	Leu	Pro	Val 315	Leu	Glu	Ser	Phe	Lys 320
Val	Ser	Phe	Leu	Ser 325	Ala	Leu	Glu	Glu	Tyr 330	Thr	Lys	Lys	Leu	Asn 335	Thr

Gln

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<210> 47
<211> 1217
<212> DNA
<213> Artificial Sequence
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<220>
<223> pT7 H6 Trip-A-Apo A-1 - AmpR plasmid

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<220>
<221> CDS
<222> (100) .. (1047)
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<223>

<400> 47

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agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac	114
Met Gly Ser His His	
1 5	
cat cac cat cac gga tcg atc cag ggt aga tct cct ggt acc gag cca	162
His His His His Gly Ser Ile Gln Gly Arg Ser Pro Gly Thr Glu Pro	
10 15 20	
cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt gtg	210
Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val Val	
25 30 35	
aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg gcc	258
Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu Ala	
40 45 50	
cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc tcc	306
Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val Ser	
55 60 65	
ctg aag gga tcc gat gaa ccc ccc cag agc ccc tgg gat cga gtg aag	354
Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys	
70 75 80 85	
gac ctg gcc act gtg tac gtg gat gtg ctc aaa gac agc ggc aga gac	402
Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp	
90 95 100	
tat gtg tcc cag ttt gaa ggc tcc gcc ttg gga aaa cag cta aac cta	450
Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu	
105 110 115	
aag ctc ctt gac aac tgg gac agc gtg acc tcc acc ttc agc aag ctg	498
Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu	
120 125 130	
cgc gaa cag ctc ggc cct gtg acc cag gag ttc tgg gat aac ctg gaa	546
Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu	
135 140 145	
aag gag aca gag ggc ctg agg cag gag atg agc aag gat ctg gag gag	594
Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu	
150 155 160 165	
gtg aag gcc aag gtg cag ccc tac ctg gac gac ttc cag aag aag tgg	642
Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp	
170 175 180	
cag gag gag atg gag ctc tac cgc cag aag gtg gag ccg ctg cgc gca	690
Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala	
185 190 195	

gag ctc caa gag ggc gcg cgc cag aag ctg cac gag ctg caa gag aag 738
 Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys
 200 205 210
 ctg agc cca ctg ggc gag gag atg cgc gac cgc gcg cgc gcc cat gtg 786
 Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val
 215 220 225
 gac gcg ctg cgc acg cat ctg gcc ccc tac agc gac gag ctg cgc cag 834
 Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln
 230 235 240 245
 cgc ttg gcc gcg cgc ctt gag gct ctc aag gag aac ggc ggc gcc aga 882
 Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg
 250 255 260
 ctg gcc gag tac cac gcc aag gcc acc gag cat ctg agc acg ctc agc 930
 Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser
 265 270 275
 gag aag gcc aag ccc gcg ctc gag gac ctc cgc caa ggc ctg ctg ccc 978
 Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro
 280 285 290
 gtg ctg gag agc ttc aag gtc agc ttc ctg agc gct ctc gag gag tac 1026
 Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr
 295 300 305
 act aag aag ctc aac acc cag taataagctt gaattccgat cgggctgcta 1077
 Thr Lys Lys Leu Asn Thr Gln
 310 315
 acaaagcccg aaaggaagct gagttggctg cctgccaccg ctgagctgag caataactag 1137
 cataaccct ctgccaccgc tgtggggcct ctaaacgggt cttgaggggt tttttgctga 1197
 aaggaggaac tatatccgat 1217

<210> 48
 <211> 316
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pT7 H6 Trip-A-Apo A-1 - AmpR plasmid

<400> 48

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1 5 10 15

Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala
 20 25 30

Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg

35	40	45
Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala		
50	55	60
Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser Pro		
65	70	75 80
Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys		
	85	90 95
Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly		
	100	105 110
Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser		
	115	120 125
Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe		
	130	135 140
Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser		
145	150	155 160
Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp		
	165	170 175
Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val		
	180	185 190
Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His		
	195	200 205
Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg		
	210	215 220
Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser		
225	230	235 240
Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu		
	245	250 255
Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His		
	260	265 270

Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg
 275 280 285

Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser
 290 295 300

Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 305 310 315

<210> 49
 <211> 1088
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 Trip-A-Apo A-1-del 43 - AmpR plasmid
 <220>
 <221> CDS
 <222> (100)..(918)
 <223>

<400> 49
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 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5
 cat cac cat cac gga tcg atc cag ggt aga tct cct ggt acc gag cca 162
 His His His His Gly Ser Ile Gln Gly Arg Ser Pro Gly Thr Glu Pro
 10 15 20
 cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt gtg 210
 Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val Val
 25 30 35
 aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg gcc 258
 Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu Ala
 40 45 50
 cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc tcc 306
 Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val Ser
 55 60 65
 ctg aag gga tcc cta aag ctc ctt gac aac tgg gac agc gtg acc tcc 354
 Leu Lys Gly Ser Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser
 70 75 80 85
 acc ttc agc aag ctg cgc gaa cag ctc ggc cct gtg acc cag gag ttc 402
 Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe
 90 95 100

tgg gat aac ctg gaa aag gag aca gag ggc ctg agg cag gag atg agc	450
Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser	
105 110 115	
aag gat ctg gag gag gtg aag gcc aag gtg cag ccc tac ctg gac gac	498
Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp	
120 125 130	
ttc cag aag aag tgg cag gag gag atg gag ctc tac cgc cag aag gtg	546
Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val	
135 140 145	
gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag aag ctg cac	594
Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His	
150 155 160 165	
gag ctg caa gag aag ctg agc cca ctg ggc gag gag atg cgc gac cgc	642
Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg	
170 175 180	
gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc ccc tac agc	690
Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser	
185 190 195	
gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct ctc aag gag	738
Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu	
200 205 210	
aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc acc gag cat	786
Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His	
215 220 225	
ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc gag gac ctc cgc	834
Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg	
230 235 240 245	
caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc ttc ctg agc	882
Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser	
250 255 260	
gct ctc gag gag tac act aag aag ctc aac acc cag taataagctt	928
Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln	
265 270	
gaattccgat ccggctgcta acaaagcccg aaaggaagct gagttggctg cctgccaccg	988
ctgagctgag caataactag cataaccct ctgccaccgc tgtggggcct ctaaaccgggt	1048
cttgaggggt tttttgctga aaggaggaac tatatccgat	1088
<210> 50	
<211> 273	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> pT7H6 Trip-A-Apo A-1-del 43 - AmpR plasmid	

<400> 50

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1 5 10 15

Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala
 20 25 30

Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg
 35 40 45

Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala
 50 55 60

Leu Gln Thr Val Ser Leu Lys Gly Ser Leu Lys Leu Leu Asp Asn Trp
 65 70 75 80

Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro
 85 90 95

Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu
 100 105 110

Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln
 115 120 125

Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu
 130 135 140

Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala
 145 150 155 160

Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu
 165 170 175

Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His
 180 185 190

Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu
 195 200 205

Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala
 210 215 220

Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala
225 230 235 240

Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys
245 250 255

Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr
260 265 270

Gln

<210> 51
<211> 1057
<212> DNA
<213> Artificial Sequence

<220>
<223> pT7 H6 Fx Cys-Apo A1 plasmid

<220>
<221> CDS
<222> (100)..(882)
<223>

<400> 51
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agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
Met Gly Ser His His
1 5

cat cac cat cac gga tcc atc gag ggt agg ggt gga tgt gat gaa ccc 162
His His His His Gly Ser Ile Glu Gly Arg Gly Gly Cys Asp Glu Pro
10 15 20

ccc cag agc ccc tgg gat cga gtg aag gac ctg gcc act gtg tac gtg 210
Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val
25 30 35

gat gtg ctc aaa gac agc ggc aga gac tat gtg tcc cag ttt gaa ggc 258
Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly
40 45 50

tcc gcc ttg gga aaa cag cta aac cta aag ctc ctt gac aac tgg gac 306
Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp
55 60 65

agc gtg acc tcc acc ttc agc aag ctg cgc gaa cag ctc ggc cct gtg 354
Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val
70 75 80 85

```

acc cag gag ttc tgg gat aac ctg gaa aag gag aca gag ggc ctg agg      402
Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg
          90                      95                      100

cag gag atg agc aag gat ctg gag gag gtg aag gcc aag gtg cag ccc      450
Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro
          105                      110                      115

tac ctg gac gac ttc cag aag aag tgg cag gag gag atg gag ctc tac      498
Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr
          120                      125                      130

cgc cag aag gtg gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc      546
Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg
          135                      140                      145

cag aag ctg cac gag ctg caa gag aag ctg agc cca ctg ggc gag gag      594
Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu
          150                      155                      160                      165

atg cgc gac cgc gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg      642
Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu
          170                      175                      180

gcc ccc tac agc gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag      690
Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu
          185                      190                      195

gct ctc aag gag aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag      738
Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys
          200                      205                      210

gcc acc gag cat ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc      786
Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu
          215                      220                      225

gag gac ctc cgc caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc      834
Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val
          230                      235                      240                      245

agc ttc ctg agc gct ctc gag gag tac act aag aag ctc aac acc cag      882
Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
          250                      255                      260

taagcatgca agcttgaatt ccgatccggc tgctaacaaa gcccgaaagg aagctgagtt      942

ggctgectgc caccgtgag ctgagcaata actagcataa cccctctgcc accgctgtgg      1002

ggcctctaaa cgggtcttga ggggtttttt gctgaaagga ggaactatat ccgat      1057

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<210> 52

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> pT7 H6 Fx Cys-Apo A1 plasmid

<400> 52

Met Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Gly
1 5 10 15

Gly Cys Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu
20 25 30

Ala Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val
35 40 45

Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu
50 55 60

Leu Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu
65 70 75 80

Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu
85 90 95

Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys
100 105 110

Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu
115 120 125

Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu
130 135 140

Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser
145 150 155 160

Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala
165 170 175

Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu
180 185 190

Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala
195 200 205

Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys
210 215 220

Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu
 225 230 235 240

Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys
 245 250 255

Lys Leu Asn Thr Gln
 260

<210> 53
 <211> 1217
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid
 <220>
 <221> CDS
 <222> (100)..(1047)
 <223>

<400> 53
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 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5
 cat cac cat cac gga tcg atc cag ggt aga tct cct ggt acc gag cca 162
 His His His His Gly Ser Ile Gln Gly Arg Ser Pro Gly Thr Glu Pro
 10 15 20
 cca acc cag aag ccc aag gcg att gta aat gcc aag gca gat gtt gtg 210
 Pro Thr Gln Lys Pro Lys Ala Ile Val Asn Ala Lys Ala Asp Val Val
 25 30 35
 aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg gcc 258
 Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu Ala
 40 45 50
 cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc tcc 306
 Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val Ser
 55 60 65
 ctg aag gga tcc gat gaa ccc ccc cag agc ccc tgg gat cga gtg aag 354
 Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys
 70 75 80 85
 gac ctg gcc act gtg tac gtg gat gtg ctc aaa gac agc ggc aga gac 402
 Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp
 90 95 100

tat gtg tcc cag ttt gaa ggc tcc gcc ttg gga aaa cag cta aac cta	450
Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu	
105 110 115	
aag ctc ctt gac aac tgg gac agc gtg acc tcc acc ttc agc aag ctg	498
Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu	
120 125 130	
cgc gaa cag ctc ggc cct gtg acc cag gag ttc tgg gat aac ctg gaa	546
Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu	
135 140 145	
aag gag aca gag ggc ctg agg cag gag atg agc aag gat ctg gag gag	594
Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu	
150 155 160 165	
gtg aag gcc aag gtg cag ccc tac ctg gac gac ttc cag aag aag tgg	642
Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Phe Gln Lys Lys Trp	
170 175 180	
cag gag gag atg gag ctc tac cgc cag aag gtg gag ccg ctg cgc gca	690
Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala	
185 190 195	
gag ctc caa gag ggc gcg cgc cag aag ctg cac gag ctg caa gag aag	738
Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys	
200 205 210	
ctg agc cca ctg ggc gag gag atg cgc gac cgc gcg cgc gcc cat gtg	786
Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val	
215 220 225	
gac gcg ctg cgc acg cat ctg gcc ccc tac agc gac gag ctg cgc cag	834
Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln	
230 235 240 245	
cgc ttg gcc gcg cgc ctt gag gct ctc aag gag aac ggc ggc gcc aga	882
Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg	
250 255 260	
ctg gcc gag tac cac gcc aag gcc acc gag cat ctg agc acg ctc agc	930
Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser	
265 270 275	
gag aag gcc aag ccc gcg ctc gag gac ctc cgc caa ggc ctg ctg ccc	978
Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro	
280 285 290	
gtg ctg gag agc ttc aag gtc agc ttc ctg agc gct ctc gag gag tac	1026
Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr	
295 300 305	
act aag aag ctc aac acc cag taataagctt gaattccgat ccggctgcta	1077
Thr Lys Lys Leu Asn Thr Gln	
310 315	
acaaagcccg aaaggaagct gagttggctg cctgccaccg ctgagctgag caataactag	1137

cataaccct ctgccaccgc tgtggggcct ctaaacgggt cttgaggggt tttttgctga 1197

aaggaggaac tatatccgat 1217

<210> 54

<211> 316

<212> PRT

<213> Artificial Sequence

<220>

<223> pT7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid

<400> 54

Met Gly Ser His His His His His Gly Ser Ile Gln Gly Arg Ser
1 5 10 15

Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala Ile Val Asn Ala
20 25 30

Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg
35 40 45

Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala
50 55 60

Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser Pro
65 70 75 80

Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys
85 90 95

Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly
100 105 110

Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser
115 120 125

Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe
130 135 140

Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser
145 150 155 160

Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp
165 170 175

Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val
 180 185 190

Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His
 195 200 205

Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg
 210 215 220

Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser
 225 230 235 240

Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu
 245 250 255

Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His
 260 265 270

Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg
 275 280 285

Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser
 290 295 300

Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 305 310 315

<210> 55
 <211> 1238
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 Trip-A-Fn-Apo A1 - AmpR plasmid

<220>
 <221> CDS
 <222> (100)..(1068)
 <223>

<400> 55
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 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5

cat cac cat cac ggt agt ggt agt gga tca atc cag ggt aga tct cct	162
His His His His Gly Ser Gly Ser Gly Ser Ile Gln Gly Arg Ser Pro	
10 15 20	
ggt acc gag cca cca acc cag aag ccc aag aag att gta aat gcc aag	210
Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys	
25 30 35	
aaa gat gtt gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg	258
Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu	
40 45 50	
gac acc ctg gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg	306
Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu	
55 60 65	
cag acg gtc tcc ctg aag gga tcc tcg ggt cat gat gaa ccc ccc cag	354
Gln Thr Val Ser Leu Lys Gly Ser Ser Gly His Asp Glu Pro Pro Gln	
70 75 80 85	
agc ccc tgg gat cga gtg aag gac ctg gcc act gtg tac gtg gat gtg	402
Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val	
90 95 100	
ctc aaa gac agc ggc aga gac tat gtg tcc cag ttt gaa ggc tcc gcc	450
Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala	
105 110 115	
ttg gga aaa cag cta aac cta aag ctc ctt gac aac tgg gac agc gtg	498
Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val	
120 125 130	
acc tcc acc ttc agc aag ctg cgc gaa cag ctc ggc cct gtg acc cag	546
Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln	
135 140 145	
gag ttc tgg gat aac ctg gaa aag gag aca gag ggc ctg agg cag gag	594
Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu	
150 155 160 165	
atg agc aag gat ctg gag gag gtg aag gcc aag gtg cag ccc tac ctg	642
Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu	
170 175 180	
gac gac ttc cag aag aag tgg cag gag gag atg gag ctc tac cgc cag	690
Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln	
185 190 195	
aag gtg gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag aag	738
Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys	
200 205 210	
ctg cac gag ctg caa gag aag ctg agc cca ctg ggc gag gag atg cgc	786
Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg	
215 220 225	
gac cgc gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc ccc	834
Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro	

230		235		240		245
tac agc gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct ctc						882
Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu						
		250		255		260
aag gag aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc acc						930
Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr						
		265		270		275
gag cat ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc gag gac						978
Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp						
		280		285		290
ctc cgc caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc ttc						1026
Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe						
		295		300		305
ctg agc gct ctc gag gag tac act aag aag ctc aac acc cag						1068
Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln						
310		315		320		
taataagctt gaattccgat ccggctgcta acaaagcccc aaaggaagct gagttggctg						1128
cctgccaccg ctgagctgag caataactag cataaccctt ctgccaccgc tgtggggcct						1188
ctaaacgggt cttgaggqgt tttttgctga aaqqaqqaac tatatccgat						1238

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<210> 56
<211> 323
<212> PRT
<213> Artificial Sequence
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<220>
<223> pT7H6 Trip-A-Fn-Apo A1 - AmpR plasmid

<400> 56

Met Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser Ile
1 5 10 15

Gln Gly Arg Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys
20 25 30

Ile Val Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu
35 40 45

Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys
50 55 60

Glu Gln Gln Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Ser Gly His
65 70 75 80

Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr
 85 90 95

Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
 100 105 110

Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp
 115 120 125

Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
 130 135 140

Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
 145 150 155 160

Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
 165 170 175

Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
 180 185 190

Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu
 195 200 205

Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu
 210 215 220

Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg
 225 230 235 240

Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala
 245 250 255

Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr
 260 265 270

His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys
 275 280 285

Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser
 290 295 300

Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu

Asn Thr Gln

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<220>
<223>   pT7H6 Trip-A-Fn-Apo A1-final - AmpR plasmid

<220>
<221>   CDS
<222>   (100)..(1068)
<223>
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<400>	57																		
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agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac																	114		
							Met	Gly	Ser	His	His								
							1					5							
cat	cac	cat	cac	ggg	agt	ggg	agt	gga	tca	atc	cag	ggg	aga	tct	cct	162			
His	His	His	His	Gly	Ser	Gly	Ser	Gly	Ser	Ile	Gln	Gly	Arg	Ser	Pro				
				10					15					20					
ggg	acc	gag	cca	cca	acc	cag	aag	ccc	aag	aag	att	gta	aat	gcc	aag	210			
Gly	Thr	Glu	Pro	Pro	Thr	Gln	Lys	Pro	Lys	Lys	Ile	Val	Asn	Ala	Lys				
			25				30				35								
aaa	gat	gtt	gtg	aac	aca	aag	atg	ttt	gag	gag	ctc	aag	agc	cgt	ctg	258			
Lys	Asp	Val	Val	Asn	Thr	Lys	Met	Phe	Glu	Glu	Leu	Lys	Ser	Arg	Leu				
			40				45				50								
gac	acc	ctg	gcc	cag	gag	gtg	gcc	ctg	ctg	aag	gag	cag	cag	gcc	ctg	306			
Asp	Thr	Leu	Ala	Gln	Glu	Val	Ala	Leu	Leu	Lys	Glu	Gln	Gln	Ala	Leu				
		55			60			65											
cag	acg	gtc	tcc	ctg	aag	gga	acc	tcg	ggg	cag	gat	gaa	ccc	ccc	cag	354			
Gln	Thr	Val	Ser	Leu	Lys	Gly	Thr	Ser	Gly	Gln	Asp	Glu	Pro	Pro	Gln				
		70			75			80			85								
agc	ccc	tgg	gat	cga	gtg	aag	gac	ctg	gcc	act	gtg	tac	gtg	gat	gtg	402			
Ser	Pro	Trp	Asp	Arg	Val	Lys	Asp	Leu	Ala	Thr	Val	Tyr	Val	Asp	Val				
				90					95					100					
ctc	aaa	gac	agc	ggc	aga	gac	tat	gtg	tcc	cag	ttt	gaa	ggc	tcc	gcc	450			
Leu	Lys	Asp	Ser	Gly	Arg	Asp	Tyr	Val	Ser	Gln	Phe	Glu	Gly	Ser	Ala				
			105				110				115								
ttg	gga	aaa	cag	cta	aac	cta	aag	ctc	ctt	gac	aac	tgg	gac	agc	gtg	498			
Leu	Gly	Lys	Gln	Leu	Asn	Leu	Lys	Leu	Leu	Asp	Asn	Trp	Asp	Ser	Val				

120	125	130	
acc tcc acc ttc agc aag ctg cgc gaa cag ctc ggc cct gtg acc cag Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln 135 140 145			546
gag ttc tgg gat aac ctg gaa aag gag aca gag ggc ctg agg cag gag Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu 150 155 160 165			594
atg agc aag gat ctg gag gag gtg aag gcc aag gtg cag ccc tac ctg Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu 170 175 180			642
gac gac ttc cag aag aag tgg cag gag gag atg gag ctc tac cgc cag Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln 185 190 195			690
aag gtg gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag aag Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys 200 205 210			738
ctg cac gag ctg caa gag aag ctg agc cca ctg ggc gag gag atg cgc Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg 215 220 225			786
gac cgc gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc ccc Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro 230 235 240 245			834
tac agc gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct ctc Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu 250 255 260			882
aag gag aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc acc Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr 265 270 275			930
gag cat ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc gag gac Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp 280 285 290			978
ctc cgc caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc ttc Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe 295 300 305			1026
ctg agc gct ctc gag gag tac act aag aag ctc aac acc cag Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln 310 315 320			1068
taataagctt gaattccgat ccggctgcta acaaagcccg aaaggaagct gagttggctg			1128
cctgccaccg ctgagctgag caataactag cataaccct ctgccaccgc tgtggggcct			1188
ctaaacgggt cttgaggggt tttttgctga aaggaggaac tatatccgat			1238

<211> 323
 <212> PRT
 <213> Artificial Sequence

<220>

<223> pT7H6 Trip-A-Fn-Apo Al-final - AmpR plasmid

<400> 58

Met Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser Ile
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Gln Gly Arg Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys
 20 25 30

Ile Val Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu
 35 40 45

Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys
 50 55 60

Glu Gln Gln Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Ser Gly Gln
 65 70 75 80

Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr
 85 90 95

Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
 100 105 110

Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp
 115 120 125

Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
 130 135 140

Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
 145 150 155 160

Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
 165 170 175

Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
 180 185 190

Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu

195	200	205
Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu		
210	215	220
Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg		
225	230	235 240
Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala		
245	250	255
Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr		
260	265	270
His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys		
275	280	285
Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser		
290	295	300
Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu		
305	310	315 320

Asn Thr Gln

<210> 59
 <211> 1238
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 Trip-A-Fn-Apo A1 final K9AK15A - AmpR plasmid

<220>
 <221> CDS
 <222> (100)..(1068)
 <223>

<400> 59	
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agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac	114
Met Gly Ser His His	
1 5	
cat cac cat cac ggt agt ggt agt gga tca atc cag ggt aga tct cct	162
His His His His Gly Ser Gly Ser Gly Ser Ile Gln Gly Arg Ser Pro	

																10																	15																	20																																		
ggt	acc	gag	cca	cca	acc	cag	aag	ccc	aag	gcg	att	gta	aat	gcc	aag																	210																																																				
Gly	Thr	Glu	Pro	Pro	Thr	Gln	Lys	Pro	Lys	Ala	Ile	Val	Asn	Ala	Lys																																																																					
																25																	30																	35																																		
gca	gat	gtt	gtg	aac	aca	aag	atg	ttt	gag	gag	ctc	aag	agc	cgt	ctg																	258																																																				
Ala	Asp	Val	Val	Asn	Thr	Lys	Met	Phe	Glu	Glu	Leu	Lys	Ser	Arg	Leu																																																																					
																40																	45																	50																																		
gac	acc	ctg	gcc	cag	gag	gtg	gcc	ctg	ctg	aag	gag	cag	cag	gcc	ctg																	306																																																				
Asp	Thr	Leu	Ala	Gln	Glu	Val	Ala	Leu	Leu	Lys	Glu	Gln	Gln	Ala	Leu																																																																					
																55																	60																	65																																		
cag	acg	gtc	tcc	ctg	aag	gga	acc	tcg	ggt	cag	gat	gaa	ccc	ccc	cag																	354																																																				
Gln	Thr	Val	Ser	Leu	Lys	Gly	Thr	Ser	Gly	Gln	Asp	Glu	Pro	Pro	Gln																																																																					
																70																	75																	80																	85																	
agc	ccc	tgg	gat	cga	gtg	aag	gac	ctg	gcc	act	gtg	tac	gtg	gat	gtg																	402																																																				
Ser	Pro	Trp	Asp	Arg	Val	Lys	Asp	Leu	Ala	Thr	Val	Tyr	Val	Asp	Val																																																																					
																90																	95																	100																																		
ctc	aaa	gac	agc	ggc	aga	gac	tat	gtg	tcc	cag	ttt	gaa	ggc	tcc	gcc																	450																																																				
Leu	Lys	Asp	Ser	Gly	Arg	Asp	Tyr	Val	Ser	Gln	Phe	Glu	Gly	Ser	Ala																																																																					
																105																	110																	115																																		
ttg	gga	aaa	cag	cta	aac	cta	aag	ctc	ctt	gac	aac	tgg	gac	agc	gtg																	498																																																				
Leu	Gly	Lys	Gln	Leu	Asn	Leu	Lys	Leu	Leu	Asp	Asn	Trp	Asp	Ser	Val																																																																					
																120																	125																	130																																		
acc	tcc	acc	ttc	agc	aag	ctg	cgc	gaa	cag	ctc	ggc	cct	gtg	acc	cag																	546																																																				
Thr	Ser	Thr	Phe	Ser	Lys	Leu	Arg	Glu	Gln	Leu	Gly	Pro	Val	Thr	Gln																																																																					
																135																	140																	145																																		
gag	ttc	tgg	gat	aac	ctg	gaa	aag	gag	aca	gag	ggc	ctg	agg	cag	gag																	594																																																				
Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr	Glu	Gly	Leu	Arg	Gln	Glu																																																																					
																150																	155																	160																	165																	
atg	agc	aag	gat	ctg	gag	gag	gtg	aag	gcc	aag	gtg	cag	ccc	tac	ctg																	642																																																				
Met	Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala	Lys	Val	Gln	Pro	Tyr	Leu																																																																					
																170																	175																	180																																		
gac	gac	ttc	cag	aag	aag	tgg	cag	gag	gag	atg	gag	ctc	tac	cgc	cag																	690																																																				
Asp	Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Glu	Met	Glu	Leu	Tyr	Arg	Gln																																																																					
																185																	190																	195																																		
aag	gtg	gag	ccg	ctg	cgc	gca	gag	ctc	caa	gag	ggc	gcg	cgc	cag	aag																	738																																																				
Lys	Val	Glu	Pro	Leu	Arg	Ala	Glu	Leu	Gln	Glu	Gly	Ala	Arg	Gln	Lys																																																																					
																200																	205																	210																																		
ctg	cac	gag	ctg	caa	gag	aag	ctg	agc	cca	ctg	ggc	gag	gag	atg	cgc																	786																																																				
Leu	His	Glu	Leu	Gln	Glu	Lys	Leu	Ser	Pro	Leu	Gly	Glu	Glu	Met	Arg																																																																					
																215																	220																	225																																		
gac	cgc	gcg	cgc	gcc	cat	gtg	gac	gcg	ctg	cgc	acg	cat	ctg	gcc	ccc																	834																																																				
Asp	Arg	Ala	Arg	Ala	His	Val	Asp	Ala	Leu	Arg	Thr	His	Leu	Ala	Pro																																																																					
																230																	235																	240																	245																	

tac agc gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct ctc 882
 Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu
 250 255 260

aag gag aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc acc 930
 Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr
 265 270 275

gag cat ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc gag gac 978
 Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp
 280 285 290

ctc cgc caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc ttc 1026
 Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe
 295 300 305

ctg agc gct ctc gag gag tac act aag aag ctc aac acc cag 1068
 Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
 310 315 320

taataagctt gaattccgat ccggctgcta acaaagcccg aaaggaagct gagttggctg 1128

cctgccaccg ctgagctgag caataactag cataaccct ctgccaccgc tgtggggcct 1188

ctaaacgggt cttgaggggt tttttgctga aaggaggaac tatatccgat 1238

<210> 60

<211> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> pT7H6 Trip-A-Fn-Apo A1 final K9AK15A - AmpR plasmid

<400> 60

Met Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser Ile
 1 5 10 15

Gln Gly Arg Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala
 20 25 30

Ile Val Asn Ala Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu
 35 40 45

Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys
 50 55 60

Glu Gln Gln Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Ser Gly Gln
 65 70 75 80

Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr

85										90					95				
Val	Tyr	Val	Asp	Val	Leu	Lys	Asp	Ser	Gly	Arg	Asp	Tyr	Val	Ser	Gln				
			100						105					110					
Phe	Glu	Gly	Ser	Ala	Leu	Gly	Lys	Gln	Leu	Asn	Leu	Lys	Leu	Leu	Asp				
		115					120					125							
Asn	Trp	Asp	Ser	Val	Thr	Ser	Thr	Phe	Ser	Lys	Leu	Arg	Glu	Gln	Leu				
	130						135					140							
Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr	Glu				
145					150					155					160				
Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala	Lys				
				165					170					175					
Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Glu	Met				
			180					185					190						
Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu	Arg	Ala	Glu	Leu	Gln	Glu				
	195						200					205							
Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	Leu	Gln	Glu	Lys	Leu	Ser	Pro	Leu				
	210					215					220								
Gly	Glu	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	His	Val	Asp	Ala	Leu	Arg				
225					230					235					240				
Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	Glu	Leu	Arg	Gln	Arg	Leu	Ala	Ala				
				245					250					255					
Arg	Leu	Glu	Ala	Leu	Lys	Glu	Asn	Gly	Gly	Ala	Arg	Leu	Ala	Glu	Tyr				
			260					265					270						
His	Ala	Lys	Ala	Thr	Glu	His	Leu	Ser	Thr	Leu	Ser	Glu	Lys	Ala	Lys				
	275						280					285							
Pro	Ala	Leu	Glu	Asp	Leu	Arg	Gln	Gly	Leu	Leu	Pro	Val	Leu	Glu	Ser				
	290					295					300								
Phe	Lys	Val	Ser	Phe	Leu	Ser	Ala	Leu	Glu	Glu	Tyr	Thr	Lys	Lys	Leu				
305					310					315					320				

Asn Thr Gln

<210> 61
 <211> 1241
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 (GS)3 Trip-A-Tn-Apo A1 AmpR plasmid

<220>
 <221> CDS
 <222> (100)..(1071)
 <223>

<400> 61
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 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5
 cat cac cat cac ggt agt ggt agt gga tca atc cag ggt aga tct cct 162
 His His His His Gly Ser Gly Ser Gly Ser Ile Gln Gly Arg Ser Pro
 10 15 20
 ggt acc gag cca cca acc cag aag ccc aag aag att gta aat gcc aag 210
 Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys
 25 30 35
 aaa gat gtt gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg 258
 Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu
 40 45 50
 gac acc ctg gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg 306
 Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu
 55 60 65
 cag acg gtc tcc ctg aag gga tcc aag gtg cac atg aag gaa ccc ccc 354
 Gln Thr Val Ser Leu Lys Gly Ser Lys Val His Met Lys Glu Pro Pro
 70 75 80 85
 cag agc ccc tgg gat cga gtg aag gac ctg gcc act gtg tac gtg gat 402
 Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp
 90 95 100
 gtg ctc aaa gac agc ggc aga gac tat gtg tcc cag ttt gaa ggc tcc 450
 Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser
 105 110 115
 gcc ttg gga aaa cag cta aac cta aag ctc ctt gac aac tgg gac agc 498
 Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser
 120 125 130

gtg acc tcc acc ttc agc aag ctg cgc gaa cag ctc ggc cct gtg acc 546
Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr
135 140 145

cag gag ttc tgg gat aac ctg gaa aag gag aca gag ggc ctg agg cag 594
Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln
150 155 160 165

gag atg agc aag gat ctg gag gag gtg aag gcc aag gtg cag ccc tac 642
Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr
170 175 180

ctg gac gac ttc cag aag aag tgg cag gag gag atg gag ctc tac cgc 690
Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg
185 190 195

cag aag gtg gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag 738
Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln
200 205 210

aag ctg cac gag ctg caa gag aag ctg agc cca ctg ggc gag gag atg 786
Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met
215 220 225

cgc gac cgc gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc 834
Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala
230 235 240 245

ccc tac agc gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct 882
Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala
250 255 260

ctc aag gag aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc 930
Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala
265 270 275

acc gag cat ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc gag 978
Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu
280 285 290

gac ctc cgc caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc 1026
Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser
295 300 305

ttc ctg agc gct ctc gag gag tac act aag aag ctc aac acc cag 1071
Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
310 315 320

taataagctt gaattccgat ccggtgcta acaaagcccg aaaggaagct gagttggctg 1131

cctgccaccg ctgagctgag caataactag cataaccct ctgccaccgc tgtggggcct 1191

ctaaacgggt cttgaggggt tttttgctga aaggaggaac tatatccgat 1241

<210> 62
<211> 324
<212> PRT

<213> Artificial Sequence

<220>

<223> pT7H6 (GS)3 Trip-A-Tn-Apo A1 AmpR plasmid

<400> 62

Met Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser Ile
1 5 10 15

Gln Gly Arg Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys
20 25 30

Ile Val Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu
35 40 45

Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys
50 55 60

Glu Gln Gln Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Lys Val His
65 70 75 80

Met Lys Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala
85 90 95

Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser
100 105 110

Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu
115 120 125

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
130 135 140

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
145 150 155 160

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
165 170 175

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
180 185 190

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
195 200 205

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro
 210 215 220

Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu
 225 230 235 240

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala
 245 250 255

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu
 260 265 270

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala
 275 280 285

Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu
 290 295 300

Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys
 305 310 315 320

Leu Asn Thr Gln

<210> 63
 <211> 1241
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 Trip-A-Tn-Apo A1-final - AmpR plasmid

<220>
 <221> CDS
 <222> (100)..(1071)
 <223>

<400> 63
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 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5
 cat cac cat cac ggt agt ggt agt gga tca atc cag ggt aga tct cct 162
 His His His His Gly Ser Gly Ser Gly Ser Ile Gln Gly Arg Ser Pro
 10 15 20

ggt acc gag cca cca acc cag aag ccc aag aag att gta aat gcc aag	210
Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys	
25 30 35	
aaa gat gtt gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg	258
Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu	
40 45 50	
gac acc ctg gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg	306
Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu	
55 60 65	
cag acg gtc tcc ctg aag gga acc aag gtg cac atg aag gaa ccc ccc	354
Gln Thr Val Ser Leu Lys Gly Thr Lys Val His Met Lys Glu Pro Pro	
70 75 80 85	
cag agc ccc tgg gat cga gtg aag gac ctg gcc act gtg tac gtg gat	402
Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp	
90 95 100	
gtg ctc aaa gac agc ggc aga gac tat gtg tcc cag ttt gaa ggc tcc	450
Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser	
105 110 115	
gcc ttg gga aaa cag cta aac cta aag ctc ctt gac aac tgg gac agc	498
Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser	
120 125 130	
gtg acc tcc acc ttc agc aag ctg cgc gaa cag ctc ggc cct gtg acc	546
Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr	
135 140 145	
cag gag ttc tgg gat aac ctg gaa aag gag aca gag ggc ctg agg cag	594
Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln	
150 155 160 165	
gag atg agc aag gat ctg gag gag gtg aag gcc aag gtg cag ccc tac	642
Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr	
170 175 180	
ctg gac gac ttc cag aag aag tgg cag gag gag atg gag ctc tac cgc	690
Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg	
185 190 195	
cag aag gtg gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag	738
Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln	
200 205 210	
aag ctg cac gag ctg caa gag aag ctg agc cca ctg ggc gag gag atg	786
Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met	
215 220 225	
cgc gac cgc gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc	834
Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala	
230 235 240 245	
ccc tac agc gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct	882
Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala	

250	255	260	
ctc aag gag aac ggc ggc gcc aga	ctg gcc gag tac cac gcc aag gcc		930
Leu Lys Glu Asn Gly Gly Ala Arg	Leu Ala Glu Tyr His Ala Lys Ala		
265	270	275	
acc gag cat ctg agc acg ctc agc	gag aag gcc aag ccc gcg ctc gag		978
Thr Glu His Leu Ser Thr Leu Ser	Glu Lys Ala Lys Pro Ala Leu Glu		
280	285	290	
gac ctc cgc caa ggc ctg ctg ccc	gtg ctg gag agc ttc aag gtc agc		1026
Asp Leu Arg Gln Gly Leu Leu Pro	Val Leu Glu Ser Phe Lys Val Ser		
295	300	305	
ttc ctg agc gct ctc gag gag tac	act aag aag ctc aac acc cag		1071
Phe Leu Ser Ala Leu Glu Glu Tyr	Thr Lys Lys Leu Asn Thr Gln		
310	315	320	
taataagctt gaattccgat ccggctgcta acaaagcccg aaaggaagct gagttggctg			1131
cctgccaccg ctgagctgag caataactag cataaccct ctgccaccgc tgtggggcct			1191
ctaaacgggt cttgaggggt tttttgctga aaggaggaac tatatccgat			1241

<210> 64

<211> 324

<212> PRT

<213> Artificial Sequence

<220>

<223> pT7H6 Trip-A-Tn-Apo A1-final - AmpR plasmid

<400> 64

Met Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser Ile
1 5 10 15

Gln Gly Arg Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys
20 25 30

Ile Val Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu
35 40 45

Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys
50 55 60

Glu Gln Gln Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Lys Val His
65 70 75 80

Met Lys Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala
85 90 95

Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser
 100 105 110

Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu
 115 120 125

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
 130 135 140

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
 145 150 155 160

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
 165 170 175

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
 180 185 190

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
 195 200 205

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro
 210 215 220

Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu
 225 230 235 240

Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala
 245 250 255

Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu
 260 265 270

Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala
 275 280 285

Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu
 290 295 300

Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys
 305 310 315 320

Leu Asn Thr Gln

<210> 65
 <211> 1241
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 Trip-A-Tn-Apo A1 final K9AK15A - AmpR plasmid

<220>
 <221> CDS
 <222> (100)..(1071)
 <223>

<400> 65
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 agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac 114
 Met Gly Ser His His
 1 5
 cat cac cat cac ggt agt ggt agt gga tca atc cag ggt aga tct cct 162
 His His His His Gly Ser Gly Ser Gly Ser Ile Gln Gly Arg Ser Pro
 10 15 20
 ggt acc gag cca cca acc cag aag ccc aag gcg att gta aat gcc aag 210
 Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala Ile Val Asn Ala Lys
 25 30 35
 gca gat gtt gtg aac aca aag atg ttt gag gag ctg aag agc cgt ctg 258
 Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu
 40 45 50
 gac acc ctg gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg 306
 Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu
 55 60 65
 cag acg gtc tcc ctg aag gga acc aag gtg cac atg aag gaa ccc ccc 354
 Gln Thr Val Ser Leu Lys Gly Thr Lys Val His Met Lys Glu Pro Pro
 70 75 80 85
 cag agc ccc tgg gat cga gtg aag gac ctg gcc act gtg tac gtg gat 402
 Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp
 90 95 100
 gtg ctg aaa gac agc ggc aga gac tat gtg tcc cag ttt gaa ggc tcc 450
 Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser
 105 110 115
 gcc ttg gga aaa cag cta aac cta aag ctg ctt gac aac tgg gac agc 498
 Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser
 120 125 130
 gtg acc tcc acc ttc agc aag ctg cgc gaa cag ctg ggc cct gtg acc 546
 Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr

135	140	145	
cag gag ttc tgg gat aac ctg gaa aag gag aca gag ggc ctg agg cag Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln 150 155 160 165			594
gag atg agc aag gat ctg gag gag gtg aag gcc aag gtg cag ccc tac Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr 170 175 180			642
ctg gac gac ttc cag aag aag tgg cag gag gag atg gag ctc tac cgc Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg 185 190 195			690
cag aag gtg gag ccg ctg cgc gca gag ctc caa gag ggc gcg cgc cag Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln 200 205 210			738
aag ctg cac gag ctg caa gag aag ctg agc cca ctg ggc gag gag atg Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met 215 220 225			786
cgc gac cgc gcg cgc gcc cat gtg gac gcg ctg cgc acg cat ctg gcc Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala 230 235 240 245			834
ccc tac agc gac gag ctg cgc cag cgc ttg gcc gcg cgc ctt gag gct Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala 250 255 260			882
ctc aag gag aac ggc ggc gcc aga ctg gcc gag tac cac gcc aag gcc Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala 265 270 275			930
acc gag cat ctg agc acg ctc agc gag aag gcc aag ccc gcg ctc gag Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu 280 285 290			978
gac ctc cgc caa ggc ctg ctg ccc gtg ctg gag agc ttc aag gtc agc Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser 295 300 305			1026
ttc ctg agc gct ctc gag gag tac act aag aag ctc aac acc cag Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln 310 315 320			1071
taataagctt gaattccgat ccggctgcta acaaagcccg aaaggaagct gagttggctg			1131
cctgccaccg ctgagctgag caataactag cataaccct ctgccaccgc tgtggggcct			1191
ctaaacgggt cttgaggggt tttttgctga aaggaggaac tatatccgat			1241

<210> 66
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>

<223> pT7H6 Trip-A-Tn-Apo A1 final K9AK15A - AmpR plasmid

<400> 66

Met Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser Ile
 1 5 10 15

Gln Gly Arg Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala
 20 25 30

Ile Val Asn Ala Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu
 35 40 45

Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys
 50 55 60

Glu Gln Gln Ala Leu Gln Thr Val Ser Leu Lys Gly Thr Lys Val His
 65 70 75 80

Met Lys Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala
 85 90 95

Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser
 100 105 110

Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu
 115 120 125

Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
 130 135 140

Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
 145 150 155 160

Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
 165 170 175

Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
 180 185 190

Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
 195 200 205

Glu Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro

210	215	220
Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu		
225	230	235 240
Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala		
	245	250 255
Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu		
	260	265 270
Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala		
	275	280 285
Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu		
	290	295 300
Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys		
305	310	315 320

Leu Asn Thr Gln

<210> 67
 <211> 1301
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6 Hp-alpha-Apo A1 - AmpR plasmid

<220>
 <221> CDS
 <222> (100)..(1131)
 <223>

<400> 67	
gatctcgatc ccgcgaaatt aatacgatac actataggga gaccacaacg gtttccctct	60
agaaataatt ttgtttaact ttaagaagga gatatacat atg gga tcg cat cac	114
	Met Gly Ser His His
	1 5
cat cac cat cac gga tcg atc cag ggt aga ggt gtg gac tca ggc aat	162
His His His His Gly Ser Ile Gln Gly Arg Gly Val Asp Ser Gly Asn	
	10 15 20
gat gtc acg gat atc gca gat gac ggc tgc ccg aag ccc ccc gag att	210
Asp Val Thr Asp Ile Ala Asp Asp Gly Cys Pro Lys Pro Pro Glu Ile	

25				30				35								
gca	cat	ggc	tat	gtg	gag	cac	tcg	gtt	cgc	tac	cag	tgt	aag	aac	tac	258
Ala	His	Gly	Tyr	Val	Glu	His	Ser	Val	Arg	Tyr	Gln	Cys	Lys	Asn	Tyr	
		40					45					50				
tac	aaa	ctg	cgc	aca	gaa	gga	gat	gga	gta	tac	acc	tta	aac	aat	gag	306
Tyr	Lys	Leu	Arg	Thr	Glu	Gly	Asp	Gly	Val	Tyr	Thr	Leu	Asn	Asn	Glu	
	55					60					65					
aag	cag	tgg	ata	aat	aag	gct	gtt	gga	gat	aaa	ctt	cct	gaa	tgt	gaa	354
Lys	Gln	Trp	Ile	Asn	Lys	Ala	Val	Gly	Asp	Lys	Leu	Pro	Glu	Cys	Glu	
70					75					80					85	
gca	gta	gct	ggg	aag	ccc	aag	aat	ccg	gca	aac	cca	gtg	cag	aga	tcc	402
Ala	Val	Ala	Gly	Lys	Pro	Lys	Asn	Pro	Ala	Asn	Pro	Val	Gln	Arg	Ser	
				90					95					100		
gat	gaa	ccc	ccc	cag	agc	ccc	tgg	gat	cga	gtg	aag	gac	ctg	gcc	act	450
Asp	Glu	Pro	Pro	Gln	Ser	Pro	Trp	Asp	Arg	Val	Lys	Asp	Leu	Ala	Thr	
			105					110					115			
gtg	tac	gtg	gat	gtg	ctc	aaa	gac	agc	ggc	aga	gac	tat	gtg	tcc	cag	498
Val	Tyr	Val	Asp	Val	Leu	Lys	Asp	Ser	Gly	Arg	Asp	Tyr	Val	Ser	Gln	
		120					125					130				
ttt	gaa	ggc	tcc	gcc	ttg	gga	aaa	cag	cta	aac	cta	aag	ctc	ctt	gac	546
Phe	Glu	Gly	Ser	Ala	Leu	Gly	Lys	Gln	Leu	Asn	Leu	Lys	Leu	Leu	Asp	
	135					140					145					
aac	tgg	gac	agc	gtg	acc	tcc	acc	ttc	agc	aag	ctg	cgc	gaa	cag	ctc	594
Asn	Trp	Asp	Ser	Val		Ser	Thr	Phe	Ser	Lys	Leu	Arg	Glu	Gln	Leu	
150					155					160					165	
ggc	cct	gtg	acc	cag	gag	ttc	tgg	gat	aac	ctg	gaa	aag	gag	aca	gag	642
Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr	Glu	
				170					175					180		
ggc	ctg	agg	cag	gag	atg	agc	aag	gat	ctg	gag	gag	gtg	aag	gcc	aag	690
Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala	Lys	
			185					190					195			
gtg	cag	ccc	tac	ctg	gac	gac	ttc	cag	aag	aag	tgg	cag	gag	gag	atg	738
Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Glu	Met	
		200					205					210				
gag	ctc	tac	cgc	cag	aag	gtg	gag	ccg	ctg	cgc	gca	gag	ctc	caa	gag	786
Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu	Arg	Ala	Glu	Leu	Gln	Glu	
	215					220					225					
ggc	gcg	cgc	cag	aag	ctg	cac	gag	ctg	caa	gag	aag	ctg	agc	cca	ctg	834
Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	Leu	Gln	Glu	Lys	Leu	Ser	Pro	Leu	
230					235					240					245	
ggc	gag	gag	atg	cgc	gac	cgc	gcg	cgc	gcc	cat	gtg	gac	gcg	ctg	cgc	882
Gly	Glu	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	His	Val	Asp	Ala	Leu	Arg	
				250					255					260		

acg cat ctg gcc ccc tac agc gac gag ctg cgc cag cgc ttg gcc gcg 930
 Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala
 265 270 275

cgc ctt gag gct ctc aag gag aac ggc ggc gcc aga ctg gcc gag tac 978
 Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr
 280 285 290

cac gcc aag gcc acc gag cat ctg agc acg ctc agc gag aag gcc aag 1026
 His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys
 295 300 305

ccc gcg ctc gag gac ctc cgc caa ggc ctg ctg ccc gtg ctg gag agc 1074
 Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser
 310 315 320 325

ttc aag gtc agc ttc ctg agc gct ctc gag gag tac act aag aag ctc 1122
 Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu
 330 335 340

aac acc cag taataagctt gaattccgat ccggtgcta acaaagcccg 1171
 Asn Thr Gln

aaaggaagct gagttggctg cctgccaccg ctgagctgag caataactag cataaccct 1231

ctgccaccgc tgtggggcct ctaaacgggt cttgaggggt tttttgctga aaggaggaac 1291

tatatccgat 1301

<210> 68

<211> 344

<212> PRT

<213> Artificial Sequence

<220>

<223> pT7H6 Hp-alpha-Apo A1 - AmpR plasmid

<400> 68

Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Gly
 1 5 10 15

Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly Cys Pro
 20 25 30

Lys Pro Pro Glu Ile Ala His Gly Tyr Val Glu His Ser Val Arg Tyr
 35 40 45

Gln Cys Lys Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly Val Tyr
 50 55 60

Thr Leu Asn Asn Glu Lys Gln Trp Ile Asn Lys Ala Val Gly Asp Lys

65					70						75					80
Leu	Pro	Glu	Cys	Glu	Ala	Val	Ala	Gly	Lys	Pro	Lys	Asn	Pro	Ala	Asn	
				85					90					95		
Pro	Val	Gln	Arg	Ser	Asp	Glu	Pro	Pro	Gln	Ser	Pro	Trp	Asp	Arg	Val	
			100					105					110			
Lys	Asp	Leu	Ala	Thr	Val	Tyr	Val	Asp	Val	Leu	Lys	Asp	Ser	Gly	Arg	
		115					120					125				
Asp	Tyr	Val	Ser	Gln	Phe	Glu	Gly	Ser	Ala	Leu	Gly	Lys	Gln	Leu	Asn	
	130					135					140					
Leu	Lys	Leu	Leu	Asp	Asn	Trp	Asp	Ser	Val	Thr	Ser	Thr	Phe	Ser	Lys	
145					150					155					160	
Leu	Arg	Glu	Gln	Leu	Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	
				165					170					175		
Glu	Lys	Glu	Thr	Glu	Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	Glu	
			180					185					190			
Glu	Val	Lys	Ala	Lys	Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	
		195					200					205				
Trp	Gln	Glu	Glu	Met	Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu	Arg	
	210					215					220					
Ala	Glu	Leu	Gln	Glu	Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	Leu	Gln	Glu	
225					230					235					240	
Lys	Leu	Ser	Pro	Leu	Gly	Glu	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	His	
				245					250					255		
Val	Asp	Ala	Leu	Arg	Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	Glu	Leu	Arg	
		260						265					270			
Gln	Arg	Leu	Ala	Ala	Arg	Leu	Glu	Ala	Leu	Lys	Glu	Asn	Gly	Gly	Ala	
		275					280					285				
Arg	Leu	Ala	Glu	Tyr	His	Ala	Lys	Ala	Thr	Glu	His	Leu	Ser	Thr	Leu	
	290					295					300					

Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu
 305 310 315 320

Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu
 325 330 335

Tyr Thr Lys Lys Leu Asn Thr Gln
 340

<210> 69
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> tetranectin (53-59) based linker
 <400> 69

Gly Thr Lys Val His Met Lys
 1 5

<210> 70
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fibronectin (2037-2049) based linker
 <400> 70

Pro Gly Thr Ser Gly Gln Gln Pro Ser Val Gly Gln Gln
 1 5 10

<210> 71
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> murine IgG3 upper hinge region-based linker
 <400> 71

Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser
 1 5 10

<210> 72
 <211> 14
 <212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker (Muller, 2000)

<400> 72

Ser Gly Gly Thr Ser Gly Ser Thr Ser Gly Thr Gly Ser Thr
1 5 10

<210> 73

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker (Muller, 2000)

<400> 73

Ala Gly Ser Ser Thr Gly Ser Ser Thr Gly Pro Gly Ser Thr Thr
1 5 10 15

<210> 74

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> flexible linker (Muller, 2000)

<400> 74

Gly Gly Ser Gly Gly Ala Pro
1 5

<210> 75

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Ubi-A-I primer #1

<400> 75

cacggatcca tcgagggtag ggggtggagat gaaccccccc agagc

45

<210> 76

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Ubi-A-I primer #2

<400> 76
tccaagctta ttactgggtg ttgagcttct tagtg 35

<210> 77
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Trip-A-A-I primer #1

<400> 77
aagggatccg atgaaccccc ccagagcccc 30

<210> 78
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Trip-A-A-I primer #2

<400> 78
tccaagctta ttactgggtg ttgagcttct tagtg 35

<210> 79
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Trip-A-I-del43 primer #1

<400> 79
aggggatccc taaagctcct tgacaactgg g 31

<210> 80
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Trip-A-I-del43 primer #2

<400> 80
tccaagctta ttactgggtg ttgagcttct tagtg 35

<210> 81
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
 <223> Ubi-Cys-A-I primer #1
 <400> 81
 ggtggatcca tcgagggtag gggatggatgt gatgaacccc ccc 43

<210> 82
 <211> 35
 <212> DNA
 <213> Artificial Sequence

Q11
conclude
 <220>
 <223> Ubi-Cys-A-I primer #2
 <400> 82
 tccaagctta ttactgggtg ttgagcttct tagtg 35

<210> 83
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6Fx-Trip-A-FN(-2)-AI primer
 <400> 83
 cgcggtatcct cgggtcagga tgaaccccccc cagagcccc 39

<210> 84
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6Fx-Trip-A-TN-AI-Bam-S primer
 <400> 84
 cgcggtatcca aggtgcacat gaaggatgaa cccccccaga gcccc 45

<210> 85
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pT7H6Fx-Trip-FN-AI primer #1
 <400> 85
 acgggtctccc tgaagggaac ctcggttcag gatg 34

<210> 86
 <211> 37
 <212> DNA

<213> Artificial Sequence

<220>

<223> pT-H6Fx-Trip-TN-AI primer

<400> 86

acggtctccc tgaagggaac caaggtgcac atgaagg

37

<210> 87

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer #1 to mutate lysine 9 from Trip-A

<400> 87

ccaaccaga agcccaaggc gaatgtaaat gcc

33

<210> 88

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer #2 to mutate lysine 9 from Trip-A

<400> 88

gtgttcacaa catctgcctt ggcatttaca atc

33

<210> 89

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer #1 to mutate lysine 15 from Trip-A

<400> 89

ggcatttaca atcgcccttg gcttctgggt tgg

33

<210> 90

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> HP-alpha-A-I cDNA fetal liver library "nonsense" primer

<400> 90

cacaagcttt ccgctagatc tctgcactgg gttagccgga ttcttggg

48

<210> 91

*Q11
Conclude*

<211> 49
<212> DNA
<213> Artificial Sequence

<220>

<223> HP-alpha-A-I fetal liver cDNA library "sense" primer

<400> 91

ggtggatcca tcgagggtag ggggtgtggac tcaggcaatg atgtcacgg

49

AG11
Boochelle